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On nucleic - nucleic search, using sw model

Run on: October 18, 2004, 11:45:41 ; Search time 2813 Seconds
(without alignments)

6758.073 Million cell updates/sec

Title: US-10-724-225-1_COPY_1_402
Perfect score: 402
Sequence: 1 ATGTGCAATACCAACATGTC.....ACCTTCAAGGTGGAGGTGAT 402

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_im: *
5: gb_iv: *
6: gb_jat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	402	100.0	646	9 AP385323
2	402	100.0	652	6 AR207094
3	402	100.0	659	9 HSA491698
4	402	100.0	729	6 A61763
5	402	100.0	729	6 AR264886
6	402	100.0	732	9 HSA430612
7	402	100.0	852	6 A44504
8	402	100.0	1476	6 A61359
9	402	100.0	1476	6 AX057138
10	402	100.0	1476	6 AX695559
11	402	100.0	1476	9 BT007258
12	402	100.0	1476	12 BT007935
13	402	100.0	2366	6 CQ717944
14	402	100.0	2372	6 AR000256
15	402	100.0	2372	6 AR009781
16	402	100.0	2372	6 AR028963
17	402	100.0	2372	6 AR154584
18	402	100.0	2372	6 BD233925
19	402	100.0	2372	6 111727

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

GenEmbl:*

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3: gb_in: *
4: gb_im: *
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6: gb_jat: *
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8: gb_pl: *
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10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

ALIGNMENTS

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21	402	100.0	2372	6 121256	I121256 Sequence 1
22	402	100.0	2372	6 123341	I123341 Sequence 2
23	402	100.0	2372	6 136472	I136472 Sequence 2
24	402	100.0	2372	6 140222	I140222 Sequence 2
25	402	100.0	2372	6 179856	I179856 Sequence 2
26	402	100.0	2372	6 186850	I186850 Sequence 2
27	402	100.0	2372	6 AR212312	AR212312 Sequence
28	402	100.0	2372	6 AR214399	AR214399 Sequence
29	402	100.0	2372	6 AX339941	AX339941 Sequence
30	402	100.0	2372	6 AX581651	AX581651 Sequence
31	402	100.0	3121	9 BC067075	BC067075 Canis fam
32	402	100.0	3121	9 AF100705	AF100705 Canis fam
33	402	100.0	3121	9 BD138075	BD138075 Antibense
34	402	100.0	3121	9 HSP33ASG	213200 H. sapiens m
35	402	100.0	3121	9 M92424	M92424 Human p53-a
36	402	100.0	3121	9 BC067077	BC067077 Homo sapi
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38	358.8	89.3	3121	9 AB031276	AB031276 Canis fam
39	358.8	89.3	3121	9 AF322416	AF322416 Canis fam
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41	355.6	88.5	3121	9 AF121140	AF121140 Equus cab
42	342	85.1	1361	9 AF093844	AF093844 Homo sapi
43	327.4	81.8	9 AF092843	AF092843 Homo sapi	
44	289.2	71.9	1470	6 AX695556	AX695556 Sequence
45	289.2	71.9	1470	10 MMU7934	U47934 Mus musculus

Query Match 100.0%; Score 402; DB 9; Length 646;
 Best Local Similarity 100.0%; Pred. No. 2.4e-93; Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 121 GTGGTGCAAAAGACACTTACTATGAAAGGGTTCTTTATCTGGCCAGAT 180
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 Db 181 ATTAGACTAACGATTATGATGAGAACACATATTGATATTGTCATATG 240
 QY 241 CTTCTAGGAGATTGTTGGTSCCAACSTCCTGTGAAAGGACAGGAAATAT 300
 Db 241 CTTCTAGGAGATTGTTGGTSCCAACSTCCTGTGAAAGGACAGGAAATAT 300
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QY 301 ACCATGATCTACGGACITGGTAGTACTGCAATCAGGAAATCATCGGACTCGGTCA 360
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 QY 361 TCTGTGAGTGAACAGGTTCACTGTGAAAGTGGGAGTAT 402
 Db 361 TCTGTGAGTGAACAGGTTCACTGTGAAAGTGGGAGTAT 402

RESULT 2
 AR207094 Locus AR207094 Definition Sequence 3 from patent US 6372490. DNA linear PAT 20-JUN-2002
 ACCESSION AR207094 VERSION AR207094.1 GI:21505896
 KEYWORDS SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 652)
 AUTHORS Nandabalan, K., Yang, M. and Schulz, V.
 TITLE Nucleic acid encoding the MDM interacting protein
 JOURNAL Patent: US 6372490-A 3 16-APR-2002;
 FEATURES source 1. .652
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 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 2.4e-93; Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCGAAATCCACATGTTGTACTAGTATGGCTGCTAACACCTCACAGATTCA 60
 Db 1 ATGTCGAAATCCACATGTTGTACTAGTATGGCTGCTAACACCTCACAGATTCA 60
 QY 61 GCTTCGGAAAGAGACCTGGTTAGCCAAAGCCATGCTTGAAGTAAAGCT 120
 Db 61 GCTTCGGAAAGAGACCTGGTTAGCCAAAGCCATGCTTGAAGTAAAGCT 120
 QY 121 GCTTCGGAAAGAGACCTGGTTAGCCAAAGCCATGCTTGAAGTAAAGCT 180
 Db 121 GCTTCGGAAAGAGACCTGGTTAGCCAAAGCCATGCTTGAAGTAAAGCT 180
 QY 181 ATTATGACTAACGATTATGATGAGAACACATATTGATATGTCATATG 240
 Db 181 ATTATGACTAACGATTATGATGAGAACACATATTGATATGTCATATG 240

RESULT 3
 HS491698 Locus HSA491698 Definition Homo sapiens mRNA for p53-binding protein alternatively spliced isoform HB67 (MDM2 gene).
 ACCESSION AJ491698 VERSION AJ491698.1 GI:21628666
 KEYWORDS alternative splicing; MDM2 gene; p53-binding protein.
 SOURCE Homo sapiens (human)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Bartel, F., Pinkert, D., Kappler, M., Bache, M., Schmidt, H. and Taubert, H.
 TITLE Alternatively and aberrantly spliced transcripts of the MDM2 mRNA occur frequently in human soft tissue sarcoma and in multiple normal tissues
 JOURNAL Unpublished
 2 (bases 1 to 659)
 REFERENCE 2 (bases 1 to 659)
 AUTHORS Bartel, F.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2002) Bartel, F., Institute for Pathology, University of Halle, Faculty of Medicine, Magdeburger St. 14, 06097 Halle, GERMANY
 FEATURES source
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /call_type="Lymphocyte"
 /gene="MDM2"
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 /product="p53-binding protein"
 /protein_id="CAD3699.1"
 /protein_id="CAD3699.1"
 /db_xref="IGI:2128657"
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Query Match 100.0%; Score 402; DB 9; Length 659;
 Best Local Similarity 100.0%; Pred. No. 2.4e-93; Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 GCTTCGGAAAGAGACCTGGTTAGCCAAAGCCATGCTTGAAGTAAAGCT 120
 QY 121 GCTTCGGAAAGAGACCTGGTTAGCCAAAGCCATGCTTGAAGTAAAGCT 180
 Db 121 GCTTCGGAAAGAGACCTGGTTAGCCAAAGCCATGCTTGAAGTAAAGCT 180
 QY 181 ATTATGACTAACGATTATGATGAGAACACATATTGATATGTCATATG 240
 Db 181 ATTATGACTAACGATTATGATGAGAACACATATTGATATGTCATATG 240

QY 121 GTGGGTGCAAAAGACACTTAACTGAAAGGGTTTTTACGTGGCCAGAT 180
 Db 121 GTGGGTGCAAAAGACACTTAACTGAAAGGGTTTTTACGTGGCCAGAT 180
 QY 181 ATTAGACTAAAGGTTATATGATGAGAACACATATGTTATGTCATGAT 240
 Db 181 ATTAGACTAAAGGTTATATGATGAGAACACATATGTTATGTCATGAT 240
 QY 241 CTTCCTAGGAGATTGTTGGCGGCCAACCTCTGTGAAGAGCAGGAAATAT 300
 Db 241 CTTCCTAGGAGATTGTTGGCGGCCAACCTCTGTGAAGAGCAGGAAATAT 300
 QY 301 ACCATGACTACAGGACTTGGTAGTACTCAATCAGCGGAATCATCGACTGGTCA 360
 Db 301 ACCATGACTACAGGACTTGGTAGTACTCAATCAGCGGAATCATCGACTGGTCA 360
 Db 384 ACCATGACTACAGGACTTGGTAGTACTCAATCAGCGGAATCATCGACTGGTCA 443
 QY 361 TCTGTGAGTGGAGACAGGGTCACTTGAGGGGGTGT 402
 Db 361 TCTGTGAGTGGAGACAGGGTCACTTGAGGGGGTGT 402
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 Db 301 ACCATGACTACAGGACTTGGTAGTACTCAATCAGCGGAATCATCGACTGGTCA 360
 Db 361 TCTGTGAGTGGAGACAGGGTCACTTGAGGGGGTGT 402
 QY 361 TCTGTGAGTGGAGACAGGGTCACTTGAGGGGGTGT 402
 Db 361 TCTGTGAGTGGAGACAGGGTCACTTGAGGGGGTGT 402
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 A61763 A61763 Sequence 3 from Patent: WO9711367. DNA linear PAT 09-MAR-1998
 LOCUS A61763
 DEFINITION Sequence 3 from Patent: WO9711367.
 ACCESSION A61763
 VERSION A61763.1 GI:3715951
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified.
 REFERENCE 1.
 AUTHORS Chene, P. and Hochkeppel, H.-K.
 TITLE ASSAY FOR IDENTIFYING INHIBITORS OF THE INTERACTION BETWEEN
 JOURNAL PROTEINS p53 AND dm2
 PATENT: WO 9711367-A 3 27-MAR-1997;
 FEATURES source
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 Best Local Similarity 100.0%; Pred. No. 2_3e-93; Mismatches 0; Indels 0; Gaps 0;
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 QY 1 ATGTCATAACACATGTGTGACTACTGATGGTGTGTTAACACCTCACAGATCCA 60
 Db 84 ATGTCATAACACATGTGTGACTACTGATGGTGTGTTAACACCTCACAGATCCA 143
 QY 61 GCTTCGGAACAGAGGCCCTGGTAGCCAAGCCATGCTTGAAGTTAAAGCT 120
 Db 144 GCTTCGGAACAGAGGCCCTGGTAGCCAAGCCATGCTTGAAGTTAAAGCT 203
 QY 121 GTGGGTGCAAAAGACACTTAACTGAAAGGGTTTTTACGTGGCCAGAT 180
 Db 204 GTGGGTGCAAAAGACACTTAACTGAAAGGGTTTTTACGTGGCCAGAT 263
 QY 181 ATTAGACTAAAGGTTATATGATGAGAACACATATGTTATGTCATGAT 240
 Db 264 ATTAGACTAAAGGTTATATGATGAGAACACATATGTTATGTCATGAT 323
 QY 241 CTTCCTAGGAGATTGTTGGCGGCCAACCTCTGTGAAGAGCAGGAAATAT 300
 Db 324 CTTCCTAGGAGATTGTTGGCGGCCAACCTCTGTGAAGAGCAGGAAATAT 383
 QY 301 ACCATGACTACAGGACTTGGTAGTACTCAATCAGCGGAATCATCGACTGGTCA 360
 Db 384 ACCATGACTACAGGACTTGGTAGTACTCAATCAGCGGAATCATCGACTGGTCA 443
 QY 361 TCTGTGAGTGGAGACAGGGTCACTTGAGGGGGTGT 402
 Db 444 TCTGTGAGTGGAGACAGGGTCACTTGAGGGGGTGT 485
 RESULT 5
 AR264886 AR264886 Sequence 3 from patent US 6492116. DNA linear PAT 10-APR-2003
 LOCUS AR264886
 DEFINITION Sequence 3 from patent US 6492116.
 ACCESSION AR264886
 VERSION AR264886.1 GI:29693255
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1.
 AUTHORS Chene, P. and Hochkeppel, H.-K.
 TITLE ASSAY for identifying inhibitors of the interaction between
 Proteins p53 and dm2
 PATENT: US 6492116-A 3 10-DEC-2002;
 FEATURES source
 CDS
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 Query Match 100.0%; Score 402; DB 6; Length 729;
 Best Local Similarity 100.0%; Pred. No. 2_3e-93; Mismatches 0; Indels 0; Gaps 0;
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 QY 1 ATGTCATAACACATGTGTGACTACTGATGGTGTGTTAACACCTCACAGATCCA 60
 Db 84 ATGTCATAACACATGTGTGACTACTGATGGTGTGTTAACACCTCACAGATCCA 143
 QY 61 GCTTCGGAACAGAGGCCCTGGTAGCCAAGCCATGCTTGAAGTTAAAGCT 120
 Db 144 GCTTCGGAACAGAGGCCCTGGTAGCCAAGCCATGCTTGAAGTTAAAGCT 203
 QY 121 GTGGGTGCAAAAGACACTTAACTGAAAGGGTTTTTACGTGGCCAGAT 180
 Db 204 GTGGGTGCAAAAGACACTTAACTGAAAGGGTTTTTACGTGGCCAGAT 263
 QY 181 ATTAGACTAAAGGTTATATGATGAGAACACATATGTTATGTCATGAT 240
 Db 264 ATTAGACTAAAGGTTATATGATGAGAACACATATGTTATGTCATGAT 323
 QY 241 CTTCCTAGGAGATTGTTGGCGGCCAACCTCTGTGAAGAGCAGGAAATAT 300
 Db 324 CTTCCTAGGAGATTGTTGGCGGCCAACCTCTGTGAAGAGCAGGAAATAT 383
 QY 301 ACCATGACTACAGGACTTGGTAGTACTCAATCAGCGGAATCATCGACTGGTCA 360
 Db 384 ACCATGACTACAGGACTTGGTAGTACTCAATCAGCGGAATCATCGACTGGTCA 443
 QY 361 TCTGTGAGTGGAGACAGGGTCACTTGAGGGGGTGT 402
 Db 444 TCTGTGAGTGGAGACAGGGTCACTTGAGGGGGTGT 485
 RESULT 6
 HS430612 HS430612 Homo sapiens mRNA for MDM2 isoform KB9. mRNA linear PRI 15-FEB-2002
 LOCUS HS430612
 DEFINITION Homo sapiens mRNA for MDM2 isoform KB9.
 ACCESSION AJ430612

VERSION	AJ430612.1	RESULT	7
KEYWORDS	Lymphocytes; MDM2 isoform KB9.	ACCESSION	A44504
SOURCE	Homo sapiens (human)	DEFINITION	Sequence 4 from Patent WO9514233.
ORGANISM	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	VERSION	A44504.1
REFERENCE	1 Bartel, F., Pinkert, D., Kappler, M., Bache, M., Schmidt, H. and Taubert, H.	LOCUS	A44504
AUTHORS	Alternatively and Aberrantly Spliced Transcripts of the MDM2-mRNA	DEFINITION	Sequence 4 from Patent WO9514233.
TITLE	Occur Frequently in Human Soft Tissue Sarcomas and in Multiple	ORGANISM	unclassified
JOURNAL	Normal Tissues	REFERENCE	1 (bases 1 to 852)
REFERENCE	Unpublished	AUTHORS	Zentgraf, H., Klein, R., Frey, M. and Martens, R.
AUTHORS	2 (bases 1 to 732)	TITLE	METHOD OF IDENTIFYING MDM2-SPECIFIC ANTIBODIES
TITLE	Direct Submission	PATENT	WO 9514233-A 4 26-MAY-1995;
JOURNAL	Submitted (112-FEB-2002) Bartel F., Institute for Pathology, University of Halle, Faculty of Medicine, Magdeburger Str. 14, 06097 Halle, GERMANY	COMMENT	DEUTSCHES KRESFORSCH (DE)
FEATURES	source	FEATURES	Other publication DE 4339533 950614
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Matches	402;	Pred.	No. 2, 3e-93;
Best local similarity	100.0%	Mismatches	0;
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Best local similarity	100.0%	Gaps	0;
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Query	RESULT 8	Query	RESULT 8
Db	A61359	Query	A61359
	LOCUS	ACCESSION	ACCESSION
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	DEFINITION	DEFINITION	DEFINITION
	Sequence 1 from Patent WO9703343.	VERSION	VERSION
	1476 bp	1	1
	DNA	1	1
	linear	linear	linear
	PAT 09-MAR-1998	PAT 09-MAR-1998	PAT 09-MAR-1998
REFERENCE	1	REFERENCE	1
AUTHORS	Tocque, B., Dubz-Poterszman, M. and Wasyluk, B.	AUTHORS	Tocque, B., Dubz-Poterszman, M. and Wasyluk, B.
TITLE	ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF CANCERS	TITLE	ANTAGONISTS OF THE ONCOGENIC ACTIVITY OF THE PROTEIN MDM2, AND USE THEREOF IN THE TREATMENT OF CANCERS
JOURNAL	Patent: WO 9709343-A 1 13-MAR-1997;	JOURNAL	Patent: WO 9709343-A 1 13-MAR-1997;

COMMENT	FEATURE	Source
RHONE POULENC RORER SA (FR) Other publication FR 2738151 970307.		
LOCATION	/location	/Qualifiers
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QTVVYQGEGSDTSDPSDEPEISLADSYKUNPPLPSHCNRWALRNNLPEK		
GKDGEISERAKUNENSTQAEEGDVPECKKTIVNDSDRESCVEENDDKITQASQSE		
DYSQPSTSSIIYSSQDVKERERETODKESVESPILLNAIEPCVICOGRPKNGCI		
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ORIGIN		
Query Match 100.0%; Score 402; DB 6; Length 1476;		
Best Local Similarity 100.0%; Pred. No. 2.3e-93;		
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY		
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1 ATGTCGAATACCAAGATGCTGTACACTGTGTTGCTGTAACCAACCTCACAGATCCA	60	
QY		
61 GCTTCGGAAACAAGAGACCCCTGGTAGACCAAGCCATTGTTGAAGTATTAAAGCT	120	
61 GCTTCGGAAACAAGAGACCCCTGGTAGACCAAGCCATTGTTGAAGTATTAAAGCT	120	
Db		
61 GCTTCGGAAACAAGAGACCCCTGGTAGACCAAGCCATTGTTGAAGTATTAAAGCT	120	
QY		
121 GRTGGTGCACAAAGAGACCTATATGAAAGGGCTTTTATCTGCCAGT 180		
121 GRTGGTGCACAAAGAGACCTATATGAAAGGGCTTTTATCTGCCAGT 180		
Db		
61 GCTTCGGAAACAAGAGACCCCTGGTAGACCAAGCCATTGTTGAAGTATTAAAGCT	120	
QY		
121 GTTGGTGCACAAAGAGACCTATATGAAAGGGCTTTTATCTGCCAGT 180		
121 GTTGGTGCACAAAGAGACCTATATGAAAGGGCTTTTATCTGCCAGT 180		
Db		
61 GCTTCGGAAACAAGAGACCCCTGGTAGACCAAGCCATTGTTGAAGTATTAAAGCT	120	
QY		
181 ATTAGACTAAAGGATTATGATGAGAGAACACATATGTTATATGTCAGATAT 240		
181 ATTAGACTAAAGGATTATGATGAGAGAACACATATGTTATATGTCAGATAT 240		
Db		
181 ATTAGACTAAAGGATTATGATGAGAGAACACATATGTTATATGTCAGATAT 240		
QY		
241 CTTCTAGTACAGGAACTTGGTAGTCACTGAGGAGAACATCGGACTCAGGTACA	360	
241 CTTCTAGTACAGGAACTTGGTAGTCACTGAGGAGAACATCGGACTCAGGTACA	360	
Db		
301 ACCATGATCTACAGGAACTTGGTAGTCACTGAGGAGAACATCGGACTCAGGTACA	360	
301 ACCATGATCTACAGGAACTTGGTAGTCACTGAGGAGAACATCGGACTCAGGTACA	360	
QY		
301 ACCATGATCTACAGGAACTTGGTAGTCACTGAGGAGAACATCGGACTCAGGTACA	360	
Db		
361 TCTGTGAGTGAGAACAGGCTCACCTGAGGTGGAGGTGAT 402		
361 TCTGTGAGTGAGAACAGGCTCACCTGAGGTGGAGGTGAT 402		
Db		
361 TCTGTGAGTGAGAACAGGCTCACCTGAGGTGGAGGTGAT 402		
RESULT 9		
AX057138	AX057138	1476 bp DNA linear PAT 17-JAN-2001
LOCUS	Sequence 14 from Patent WO0075184.	
DEFINITION		
ACCESSION	AX057138	
VERSION	AX057138.1	GI:12309959
KEYWORDS	Homo sapiens (human)	
SOURCE		
ORGANISM	Homo sapiens (human)	
REFERENCE		
AUTHORS	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		
JOURNAL		
FEATURES		
source	1. .1476	
	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	
FEATURES		
LOCATION		
1. Zhang, H., Tsvetkov, L.M. and Kondo, T. Modulation of protein levels using the scf complex		
Patent: WO 0075184-A 14-DEC-2000; YALE UNIVERSITY (US)		
Location/Qualifiers		
CDS		
1. .1476		
/organism="Homo sapiens"		
/mol_type="unassigned DNA"		
REFERENCE		
AUTHORS	Morris, D.W. and Engelhard, B.K.	
TITLE	Novel compositions and methods for cancer	
JOURNAL	Patent: WO 03098583-A 1186 30-JAN-2003; Sagres Discovery (US)	
FEATURES		
source	1. .1476	
	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	
RESULT 10		
AX95559	AX95559	1476 bp DNA linear PAT 31-MAR-2003
LOCUS	Sequence 1186 from Patent WO03098583.	
DEFINITION		
ACCESSION	AX95559	
VERSION	AX95559.1	GI:29418711
KEYWORDS		
SOURCE		
ORGANISM	Homo sapiens (human)	
REFERENCE		
AUTHORS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE		
JOURNAL		
FEATURES		
source	1. .1476	
	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	

Cloning of human full-length CDSs in BD Creator™ System Donor vector	Chelen, M. and Farmer, A.
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1476)
AUTHORS	Kalmine, N., Chen, X., Rolfs, A., Halleck, A., Hines, J., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M., and Farmer, A.
TITLE	Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA
JOURNAL	This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion™ cloning system between the Sall and HindIII sites of the pDON-DUAL vector. Additional sequences in the clone: 'ACC' after the Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.
COMMENT	Clone distribution: http://bioinfo.clontech.com/otfclones .
FEATURES	<p>source</p> <p>1. 1476 /organism="synthetic construct" /mol_type="mRNA" /db_xref="taxon:32630"</p> <p>/clone="GH0020311_0"</p> <p>/clone_1ib="BD Creator™ CDS Library derived from MGC collection"</p> <p>/lab_host="DH5alpha T1 resistant"</p> <p>/note="Vector: pDON-Dual"</p> <p>1. >1476 /note="Mutations: 1475:Stop->Leu" /codon_start=1</p> <p>/transl_table=11</p> <p>/product="Homo sapiens Mdn2, transformed 3T3 cell double minute 2, p53 binding protein (mouse)" /protein_id="AAU36607.1"</p> <p>/protein_xref="GI: 30584709"</p> <p>/translation="MONTINMSVPTGAVITSQIPASBQETLVRPKPLKLKILKSVQAO KDTYTMKEVFLVFLQGIMTKYLDKQHQTVCNSDLDLGDIFGVRSFSVKERKTYM KTYNLUVWNOESSGSGTYSVNECNLEGSSDOKVOLQEBKQSSVSPSS RRAISSETEENSDLSGERQRKHKSDSISFDESILACVIREICCRSSSESTGT PSNPDIADAGVSEHSGWMDLSDVSDFPVEVESEDLSBEGQESDDBEVY QVTYVOAGESDTSFSEPELSLADWYKSCNEMPPLSHCRNRLWENLWBDK GKDKEISIKAJUNSTQAEFGFDPKKTI VNDSSRESCVEENDDKITQASQSESE DYSQSTSSSIYSSQEDVKEFEREFTQDKESVSSSLPLNAIEPCVICOVRPNQCI VHGKTCMLMACFTCAKLUKRENKPVCVRQPIQIVLTYFL"</p>
CDS	<p>ORIGIN</p> <p>Query Match 100.0%; Score 402; DB 12; Length 1476; Best Local Similarity 100.0%; Pred. No. 2.3e-93; Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 1 ATGTGCAATACCAACATGTGTACTACTGTATGGTGTAAACCCCTCACAGATCCA 60 Db 305 ATGTGCAATACCAACATGTGTACTACTGTATGGTGTAAACCCCTCACAGATCCA 365</p> <p>QY 61 GCTTGGAAACAGAGACCTGTAGACCAAGAACATGGTGTAAACCCCTCACAGATCCA 120 Db 366 GCTTGGAAACAGAGACCTGTAGACCAAGAACATGGTGTAAACCCCTCACAGATCCA 425</p> <p>QY 121 GTTGGTGCACAAAGACACTTATACATGAGAGGTCTTTATCTGGCACTAT 180 Db 426 GTTGGTGCACAAAGACACTTATACATGAGAGGTCTTTATCTGGCACTAT 485</p> <p>QY 181 ATATGACTAACGATTATATGAGAGAACACATATTGTATATGTTCAATGAT 240 Db 486 ATATGACTAACGATTATATGAGAGAACACATATTGTATATGTTCAATGAT 545</p> <p>QY 241 CTCTCTAGGAGATTGTGCGGCGCAAGCTCTCTGTGAAAGAACAGGAATATAT 300 Db 546 CTCTCTAGGAGATTGTGCGGCGCAAGCTCTCTGTGAAAGAACAGGAATATAT 605</p> <p>QY 301 ACCATGACTAACGAACTGTGAGTAGTCACTAGCAGAACATCGGACTCGGTAC 360 Db 606 ACCATGACTAACGAACTGTGAGTAGTCACTAGCAGAACATCGGACTCGGTAC 665</p> <p>QY 361 TCTGTGAGTGAACAGGTGTACCTGTGAGGTGGAGGTGTACATCGGACTCGGTAC 402 Db 666 TCTGTGAGTGAACAGGTGTACCTGTGAGGTGGAGGTGTACATCGGACTCGGTAC 707</p>
RESULT	14
Db	AR000256
LOCUS	AR000256
DEFINITION	Sequence 2 from patent US 5756338.
ACCESSION	AR000256

VERSION AR000256.1 GI:3962787

KEYWORDS Unknown.

ORGANISM Unknown.

REFERENCE 1. (bases 1 to 2372) Burrell,M., Hill,D.E., Kinzler,K.W. and Vogelstein,B. Method of diagnosing Neoplastic disease by detecting increased expression of human MDM2 protein

AUTHORS

TITLE Patent: US 573638-A 2 07-APR-1998;

JOURNAL

FEATURES Location/Qualifiers

SOURCE 1. .2372 /organism="unknown" /mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 402; DB 6; Length 2372; Best Local Similarity 100.0%; Pred. No. 2.2e-93; Mismatches 0; Indels 0; Gaps 0; Matches 402; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 ATGTCGAATACCAACAGCTGTAACCTACTGTTGTTGACCACTCACAGATCCA 60

Db 312 ATGTCGAATACCAACAGCTGTAACCTACTGTTGTTGACCACTCACAGATCCA 371

QY 61 GCTCGGACACAGAGACCCCTGGTAGCCAAAGCCATGCTTGAAGTTAAAGCT 120

Db 372 GCTCGGACACAGAGACCCCTGGTAGCCAAAGCCATGCTTGAAGTTAAAGCT 431

Db 312 ATGTCGAATACCAACAGCTGTTGACCTACTGATGGTGCCTAACGATTCGA 60

QY 61 GCTCGGACACAGAGACCCCTGGTAGCCAAAGCCATGCTTGAAGTTAAAGCT 121

Db 372 GCTCGGACACAGAGACCCCTGGTAGCCAAAGCCATGCTTGAAGTTAAAGCT 180

Db 432 GTGGTGACACAAAGACACTATACATGATGGTGCCTAACGACCTCACAGATCCA 371

QY 121 GTGGTGACACAAAGACACTATACATGATGGTGCCTAACGACCTCACAGATCCA 180

Db 432 GTGGTGACACAAAGACACTATACATGATGGTGCCTAACGACCTCACAGATCCA 491

QY 492 ATTATGACTAACGATATATGATGAGAACGACATATGTTAAGT 240

Db 492 ATTATGACTAACGATATATGATGAGAACGACATATGTTAAGT 551

QY 241 CTTCTAGGAGTTGTTGGCGTGCACGCTCTGTAAGAGCTCTTGCAAGAGCCAGGAAATTAT 300

Db 552 CTTCTAGGAGTTGTTGGCGTGCACGCTCTGTAAGAGCTCTTGCAAGAGCCAGGAAATTAT 611

QY 181 ATTATGACTAACGATTATGATGAGAACGACACATATGTTAATGTTCAATGAT 240

Db 492 ATTATGACTAACGATTATGATGAGAACGACACATATGTTAATGTTCAATGAT 551

QY 241 CTTCTAGGAGTTGTTGGCGTGCACGCTCTGTAAGAGCTCTTGCAAGAGCCAGGAAATTAT 300

Db 552 CTTCTAGGAGTTGTTGGCGTGCACGCTCTGTAAGAGCTCTTGCAAGAGCCAGGAAATTAT 611

QY 301 ACCATGATTCACAGAACTTGGTAGTGTCAATCAGCAGGATCATCGGACTCAGGTACA 360

Db 612 ACCATGATTCACAGAACTTGGTAGTGTCAATCAGCAGGATCATCGGACTCAGGTACA 671

QY 361 TCTGTGAGTGAGAACAGGTGTCACCTGAGGGTGGAGT 402

Db 672 TCTGTGAGTGAGAACAGGTGTCACCTGAGGGTGGAGT 713

RESULT 15

AR009781

LOCUS AR009781

DEFINITION Sequence 2 from patent US 5736455.

ACCESSION AR009781

VERSION AR009781.1 GI:3968586

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1. (bases 1 to 2372) Kinzler,K.W. and Vogelstein,B. Amplification of human MDM2 gene in human tumors

AUTHORS

TITLE Patent: US 5736455-A 2 26-MAY-1998;

JOURNAL

FEATURES Location/Qualifiers

SOURCE 1. .2372 /organism="unknown" /mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 402; DB 6; Length 2372; Best Local Similarity 100.0%; Pred. No. 2.2e-93; Mismatches 0; Indels 0; Gaps 0; Matches 402; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: October 18, 2004, 11:45:41 ; Search time 982 Seconds
(without alignments)
2148.948 Million cell updates/sec

Title: US-10-724-225-1_COPY_1_402
Perfect score: 402
Sequence: 1 ATGTCGATACCAACATGTC.....ACCTTGAGGTGGAGGTGAT 402
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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1: geneseqn1980s:/*
2: geneseqn1990s:/*
3: geneseqn2000s:/*
4: geneseqn2011a:/*
5: geneseqn2001b:/*
6: geneseqn2002a:/*
7: geneseqn2002b:/*
8: geneseqn2003a:/*
9: geneseqn2003b:/*
10: geneseqn2003c:/*
11: geneseqn2004a:/*
12: geneseqn2004b:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	402	100.0	652	Aaa75042
2	402	100.0	852	Aaq92515
3	402	100.0	852	Aaq92515 Human enco
4	402	100.0	1476	AAT61637 Human dou
5	402	100.0	1476	AAT61637 Murine do
6	402	100.0	1476	AAC84196 Human MDM
7	402	100.0	1476	AAC84196 Human MDM
8	402	100.0	1476	ADB72406 Human MDM
9	402	100.0	1476	ADB72406 Human MDM
10	402	100.0	2371	ADP9196 Human MDM
11	402	100.0	2372	ADP9196 Human MDM
12	402	100.0	2372	ADT45151 Human MDM
13	402	100.0	2372	ADT66310 Human MDM
14	402	100.0	2372	ADT66310 Human MDM
15	402	100.0	2372	AAV20549 Human MDM
16	402	100.0	2372	AAV20549 Human MDM
17	402	100.0	2372	AAV20549 Human MDM
18	402	100.0	2372	AAV20549 Human MDM
19	402	100.0	2372	AAV20549 Human MDM
20	402	100.0	2372	AAV20549 Human MDM
21	402	100.0	2372	AAV20549 Human MDM

Result No.	Score	Query Match Length	DB ID	Description	Location/Qualifier _B
Key	FT	FT	FT	FT	FT
	FT	FT	FT	FT	FT
1	402	100.0	652	Aaa75042 cDNA enco	1..652
2	402	100.0	852	Aaq92515 Human dou	/tag= a /transl_except= (pos: 172..177, aa: Gln) /note= "partial sequence"
3	402	100.0	852	Aaq92515 Human dou	
4	402	100.0	1476	AAT61637 Human dou	
5	402	100.0	1476	AAC84196 Human MDM	
6	402	100.0	1476	ADB72406 Human MDM	
7	402	100.0	1476	ADB72406 Human MDM	
8	402	100.0	1476	ADP9196 Human MDM	
9	402	100.0	2371	ADP9196 Human MDM	
10	402	100.0	2372	ADP9196 Human MDM	
11	402	100.0	2372	ADP9196 Human MDM	
12	402	100.0	2372	ADT45151 Human MDM	
13	402	100.0	2372	ADT66310 Human MDM	
14	402	100.0	2372	ADT66310 Human MDM	
15	402	100.0	2372	AAV20549 Human MDM	
16	402	100.0	2372	AAV20549 Human MDM	
17	402	100.0	2372	AAV20549 Human MDM	
18	402	100.0	2372	AAV20549 Human MDM	
19	402	100.0	2372	AAV20549 Human MDM	
20	402	100.0	2372	AAV20549 Human MDM	
21	402	100.0	2372	AAV20549 Human MDM	

Query Match 100.0%; Score 402; DB 4; Length 1476;
 Best Local Similarity 100.0%; Pred. No. 5e-10; Matches 402; Conserv. 0; Mismatches 0; Indels 0; Gaps 0; Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCATAACCAACAGTCGTGACTACTGATGGTGTGAAACCTCACAGATCCA 60
 Db 1 ATGTCATAACCAACAGTCGTGACTACTGATGGTGTGAAACCTCACAGATCCA 60

QY 181 ATATGACTAACGATTATGATGAGAACACATATGATATGTTCAATGAT 240
 Db 181 ATATGACTAACGATTATGATGAGAACACATATGATGGTGTGAAACCTCACAGATCCA 60

QY 241 CTCTTAGGAGATTGTTGGGTGCAAGCTCTGTGAAAGAGCACAGGAAATAT 300
 Db 241 CTCTTAGGAGATTGTTGGGTGCAAGCTCTGTGAAAGAGCACAGGAAATAT 300

QY 301 ACCATGACTACAGAACTTGGTAGTCAATAGCAGGAATCATCGACTGGTACA 360
 Db 301 ACCATGACTACAGAACTTGGTAGTCAATAGCAGGAATCATCGACTGGTACA 360

QY 361 TCTGTGAGTGAACAGGTGTCACCTGAAAGGGAGT 402
 Db 361 TCTGTGAGTGAACAGGTGTCACCTGAAAGGGAGT 402

RESULT 5
 AAC84596
 ID AAC84596 standard; DNA; 1476 BP.

XX AAC84596;
 AC AAC84596;
 DT 02-APR-2001 (first entry)
 XX DE Human MDM2 protein encoding DNA.
 KW S-Phase kinase associated protein; SKP1; SKP2; SKP2-like protein; 2P;
 KW Cul-1; cullin; CDC33; p27; cyclin E; Max; Mad; c-Myc; MDM2; p33; Bax;
 KW Bad; Bcl-1-2; tumour; cytostatic; ds.
 OS Homo sapiens.
 WO20073184-A1.

XX PD 14-DEC-2000.
 XX PF 05-JUN-2000; 2000WO-US015449.
 XX PR 04-JUN-1999; 99US-0137494P.
 XX PA (UYA) UNIV YALE.
 XX PI Zhang H, Tsvetkov IM, Kondo T;
 XX DR WPI; 2001-061703/7.
 XX P-PSDB; PAB4284.

PT Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-Phase kinase associated proteins 1, 2 and cullin/CDC33 proteins.

XX PS Example; Page 93-95; 162pp; English.

XX CC The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKP1, SKP2), SKP2-like proteins (2P) and CUL-1 (a member of the cullin/ CDC33 family of proteins). The method is useful for altering the level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p33, Bax, Bad or Bcl-2 polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for treating tumours

XX SQ Sequence 1476 BP; 491 A; 259 C; 332 G; 394 T; 0 U; 0 Other;

RESULT 6
 ADA02668
 ID ADA02668 standard; cDNA; 1476 BP.

XX AC ADA02668;
 XX DT 06-NOV-2003 (first entry)
 XX DE Human MDM2 carcinoma associated coding sequence, SEQ ID NO:1186.
 KW Human; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukemia; cytostatic; gene therapy; drug screening; gene; ss.
 KW OS Homo sapiens.
 XX PN WO2003057146-A2.
 XX PD 17-JUL-2003.
 XX PF 26-DEC-2002; 2002WO-US041414.
 XX PR 26-DEC-2001; 2001US-00035032.
 XX PA (SAGR-) SAGRES DISCOVERY.
 XX PI Morris DM;
 XX DR WPI; 2003-587068/55.

XX PT New recombinant nucleic acid encoding carcinoma associated protein, useful for preparing compositions for treating carcinomas.

XX PS Claim 1; SEQ ID NO 1186; 245pp; English.

XX CC The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482; ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically

XX
OS Homo sapiens.
XX
PN WO2003039484-A2.
XX
PD 15-MAY-2003.
XX
PP 08-NOV-2002; 2002WO-US036071.
XX
PR 08-NOV-2001; 2001US-00052482.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PT Morris DW, Engelhard BK;
XX
DR WPI; 2003-441462/41.
XX
PT New carcinoma associated nucleic acids and proteins, useful for screening
PT drug candidates, or for diagnosing and treating carcinomas, e.g.
XX lymphoma, breast cancer, prostate cancer or leukemia.
PS
XX
CC This invention relates to novel recombinant nucleic acids for use in
CC diagnosis and treatment of cancer, especially carcinomas, as well as the
CC use of compositions in screening methods. The compositions of the
CC invention may have cytostatic activity whilst the disclosed sequences may
CC be useful for gene therapy. The carcinoma associated nucleic acids and
CC proteins are useful for diagnosing and treating carcinomas, for example
CC lymphoma, breast cancer, prostate cancer or leukaemia, or for screening
CC drug candidates or bioactive agents capable of binding to, or modulating
CC the activity of, a carcinoma associated protein. The present sequence is
CC the coding DNA sequence of the human MDM2 gene which is a carcinoma
XX associated gene of the invention.
SQ Sequence 1476 BP; 491 A; 259 C; 332 G; 394 T; 0 U; 0 Other;
Query Match 100.0%; Score 402; DB 10; Length 1476;
Best Local Similarity 100.0%; Pred. No. 2; Se-105; Length 1476;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCAATACCAACAGATGCTGACTACTGATGATGCTGCTAACACCTCCACAGATTCA 60
Db 1 ATGGCAATACCAACAGATGCTGACTACTGATGATGCTGCTAACACCTCCACAGATTCA 60
QY 61 GCTTGGAAAGAGAGACCTGTTGACCAAGCCATTGCTTGAAGTTAAAGCT 120
Db 61 GCTTGGAAAGAGAGACCTGTTGACCAAGCCATTGCTTGAAGTTAAAGCT 120
QY 121 GTTGGTGCACAAAGAGACTTATCTATGAAAGGTTTTATCTGGCCAGAT 180
Db 121 GTTGGTGCACAAAGAGACTTATCTATGAAAGGTTTTATCTGGCCAGAT 180
QY 181 ATTAGACTAACGTTATGAGAACACACATTTGATATGTTCAATGAT 240
Db 181 ATTAGACTAACGTTATGAGAACACATTTGATATGTTCAATGAT 240
QY 241 CTCTAGGAGATTGTTGGGTGCCAAGGTTCTGTGAAGAGCACAGAAATAT 300
Db 241 CTCTAGGAGATTGTTGGGTGCCAAGGTTCTGTGAAGAGCACAGAAATAT 300
QY 301 ACCATGATCAGAACGAGTTGTTGAGGAACTCGACGACTAGGTACA 360
Db 301 ACCATGATCAGAACGAGTTGTTGAGGAACTCGACGACTAGGTACA 360
QY 361 TCTGTGAGTGGAGAACAGGGTCACTTGAGGTGGAGCT 402
Db 361 TCTGTGAGTGGAGAACAGGGTCACTTGAGGTGGAGCT 402
ID ADN71935
RESULT 9
ADN71935 standard; cDNA; 2371 BP.

XX
AC ADN71935;
XX
DT 12-AUG-2004 (first entry)
XX
DE MDM2 encoding cDNA SEQ ID NO:21.
XX
KW kinase pathway inhibitor; anti-prostate cancer;
KW mitogen-activated protein kinase pathway inhibitor;
KW MAP kinase pathway inhibitor; prostate cancer inhibitor;
KW phosphatidylinositol 3-kinase/Akt kinase pathway;
KW PI3K/Akt kinase pathway; cytostatic; MAP kinase inhibitor;
KW phosphatidylinositol 3-kinase/Akt kinase inhibitor;
KW PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;
KW MDM2; gene; ss.
XX
OS Unidentified.
XX
PN WO2004041185-A2.
XX
PD 21-MAY-2004.
XX
PP 31-OCT-2003; 2003WO-US034636.
XX
PR 31-OCT-2002; 2002US-0423340P.
XX
PA (UTRPP) UNIV ROCHESTER.
XX
PI Chang C, Lee Y, Lin W;
XX
DR WPI; 2004-390508/36.
XX
PT P-PSDB; ADN71936.
XX
CC Composition useful in the treatment of e.g. prostate cancer comprises a
CC kinase pathway inhibitor and an anti-prostate cancer compound.
XX
PS Disclosure; SEQ ID NO 21; 118pp; English.
XX
The present invention describes a composition (C1) which comprises a
CC kinase pathway inhibitor (a) and an anti-prostate cancer compound (b).
CC Also described: (1) identification of a mitogen-activated protein (MAP)
CC kinase pathway inhibitor involving incubating an anti-androgen or a
CC library of molecules with a cell containing an activatable MAP kinase
CC pathway and selecting the molecules which inhibit the activation of the
CC MAP kinase pathway, and (2) identification of a prostate cancer inhibitor
CC involving incubating a cell with hydroxyflutamide and potential
CC inhibitor, and assaying the level of activation of MAP kinase pathway or
CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway. C1 has
CC cytostatic activity, and can be used as a MAP kinase inhibitor,
CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase inhibitor, and androgen
CC cancer; for identifying a MAP kinase pathway inhibitor; for identifying a
CC prostate cancer inhibitor; and for reducing the number of prostate cancer
CC cells in a sample. The composition C1 provides effective combination
CC therapy as compared to prior therapies. The present sequence encodes
CC MDM2, which is used in the exemplification of the present invention.
XX
SQ Sequence 2371 BP; 698 A; 490 C; 541 G; 642 T; 0 U; 0 Other;
Query Match 100.0%; Score 402; DB 12; Length 2371;
Best Local Similarity 100.0%; Pred. No. 3; Se-105; Length 2371;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCAATACCAACAGATGCTGACTACTGATGATGCTGCTAACACCTCCACAGATTCA 60
Db 311 ATGGCAATACCAACAGATGCTGACTACTGATGATGCTGCTAACACCTCCACAGATTCA 370

Db 371 |||||GTTGGGAAAGAGACCTCTGGTTAGACCAAGCCATTGTTGAGTTAAAGCT 430
 CC suppression of cellular transformation. Inactivation of the p53 gene has
 CC been implicated in the formation, or progression of a wide variety of
 CC carcinoma. Polypeptides containing at least amino acids 11-41 of p53, or
 CC the DNA encoding these, may be used to inhibit the growth of tumour cells
 CC containing MDM2 gene amplification. (Updated on 25-MAR-2003 to correct PN
 field.)

Db 121 GTTGGGCAAAAGACATATAGTAAAGGTTCTTTATCTGGCCAGAT 180
 CC

Db 431 GTTGGGCAAAAGACATATAGTAAAGGTTCTTTATCTGGCCAGAT 490
 CC

QY 181 ATTAGACTAACGATATTATGAGAAAGCAACACATATGTTGTCATGAT 240
 XX

Db 491 ATTAGACTAACGATATTATGAGAAAGCAACACATATGTTGTCATGAT 550
 SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
 Query Match 100.0%; Score 402; DB 2; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 3e-106;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 241 CTTCCTAGGAAATTGTTGGCTGCACAGCTCTCTGTGAGAGCACGAAATAT 300
 XX

Db 551 CTTCCTAGGAAATTGTTGGCTGCACAGCTCTCTGTGAGAGCACGAAATAT 610
 SQ

QY 301 ACCATGATCTACAGGAACTTGTAGTACTATCAGCAGATCATGGACTCAGTCA 360
 XX

Db 611 ACCATGATCTACAGGAACTTGTAGTACTATCAGCAGATCATGGACTCAGTCA 670
 SQ

QY 361 TCTGTGAGTGAACAGGGTGCACCTTGAAAGGTGGAGTAT 402
 XX

Db 671 TCTGTGAGTGAACAGGGTGCACCTTGAAAGGTGGAGTAT 712
 SQ

RESULT 10

AAQ49891 ID AAQ49891 standard; cDNA; 2372 BP.

XX AC AAQ49891;

XX DT 25-MAR-2003 (revised)
 05-MAY-1994 (first entry)

XX DE Human MDM2 gene.

XX KW p53 gene; tumour suppressor gene; regulation; cellular proliferation;
 cellular transformation; carcinoma; human; tumour; MDM2; inhibition;
 gene amplification; ss.

XX OS Homo sapiens.

PH Key CDS Location/Qualifiers
 312..1787
 /*tag= a
 /product= "Human MDM2"

FT CDS

FT PT W09320238-A2.

XX PN

XX PD 14-OCT-1993.

XX PP 07-APR-1993; 93WO-US003199.

XX PR 07-APR-1992; 92US-00867840.

XX PR 23-JUN-1992; 92US-00903103.

XX PA (UWJO) UNIV JOHNS HOPKINS.

XX PI Burrell M, Hill DE, Kinzler KW, Vogelstein B;

XX DR WPI; 1993-33694/42.

DR P-PSDB; MAR42175.

XX PT Diagnosing neoplasia from amplification of MDM2 gene - or elevated gene expression, also new DNA, MDM2 protein, antibodies and treatment of sarcoma by inhibiting MDM2 expression.

XX PS Claim 19; Fig 1; 75pp; English.

CC This sequence represents the MDM2 gene. Amplification of this gene is diagnostic of neoplasia or the potential for neoplasia. The protein encoded by this gene interacts with the product of the p53 gene. p53 is a tumour suppressor gene and encodes a protein which appears to be a member of a group of proteins which regulate normal cellular proliferation and

RESULT 11

AAQ4589 ID AAQ4589 standard; cDNA; 2372 BP.

XX AC AAQ4589;

XX DT 16-OCT-2003 (revised)
 01-NOV-1995 (first entry)

XX DE Human MDM2 gene.

XX KW MDM2; Barcoma; diagnostic; DNA probe; ss.

XX OS Homo sapiens; (cell line CaCo-2).

PH Key CDS Location/Qualifiers
 312..1784
 /*tag= a

FT CDS

FT PT XX US5420263-A.

XX PN XX

XX PD 30-MAY-1995.

XX PR 07-APR-1993; 93US-00044619.

XX PF 07-APR-1992; 92US-00867840.

XX PR 23-JUN-1992; 92US-00903103.

XX PA (UWJO) UNIV JOHNS HOPKINS.

XX PI Vogelstein B, Kinzler KW;

XX
WPI; 1995-206312/27.
DR
P-PSDB; AAR76696.
XX
New human MDM2 cDNA - used to develop prods. for use in the diagnosis and
treatment of tumours.
XX
PS
Claim 1; Col 19-24; 34pp; English.
The human MDM2 gene is genetically altered (i.e. amplified) in human
tumour cells. Detecting that the gene has become amplified or detecting
increased gene product expression (using probes, proteins, antibodies and
inhibitors) allows diagnosis and therapy of cancers such as colorectal
carcinoma, lung cancer and chronic myelogenous leukaemia. The human MDM2
protein binds to human p53 and allows the cell to escape from p53-
regulated growth. (updated on 16-OCT-2003 to standardise OS field)
XX
Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3e-106; Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ATGNGCAATTCACAGATGTGTACTACTGATGGTGTGTAACCACTTCACAGATTCA 60
Db 312 ATGTCGAATTCACAGATGTGTACTACTGATGGTGTGTAACCACTTCACAGATTCA 371
Oy 61 GCTTCGGAAAGAGACCTGGTGTGACCAAGAACGATGCTTGTGAAGTATTAAGCT 120
Db 372 GCTTCGGAAAGAGACCTGGTGTGACCAAGAACGATGCTTGTGAAGTATTAAGCT 431
Oy 121 GTGCGTGACAAAGACACTTACTATGAGAGGTCTTTTACTGGCCAGAT 180
Db 432 GTGCGTGACAAAGACACTTACTATGAGAGGTCTTTTACTGGCCAGAT 491
Oy 181 ATTAGACTAAACGATTATATGAGAGAACACATAATGTTATATGGTCATGAT 240
Db 492 ATTAGACTAAACGATTATATGAGAGAACACATAATGTTATATGGTCATGAT 551
Oy 241 CTCTAGGAGATTGTTGGGTGCGTCAAGCTTCCTGTGAAAGGACAGGAAATAT 300
Db 552 CTCTAGGAGATTGTTGGGTGCGTCAAGCTTCCTGTGAAAGGACAGGAAATAT 611
Oy 301 ACCATGATCTACAGAACTTGTAGTGTAACTAGCAGGAACTCGGACTCGGTCA 360
Db 612 ACCATGATCTACAGAACTTGTAGTGTAACTAGCAGGAACTCGGACTCGGTCA 671
Oy 361 TCTGAGTGAGAACAGGTGCACTTGAGGTTGGAGTAT 402
Db 672 TCTGAGTGAGAACAGGTGCACTTGAGGTTGGAGTAT 713

RESULT 12
AAT45151
ID AAT45151 standard; cDNA; 2372 BP.
XX
AAT45151;
DT 25-MAR-2003 (revised)
28-JAN-1997 (first entry)
DE Human MDM-2 gene cDNA clone, involved in tumour-development.
KW p53; MDM-2; binding-inhibitor; identification; tumour; cancer; neoplasia;
KW antibody fusion protein; therapy; ds.
XX
OS Homo sapiens.
XX
Key location/Qualifiers
PH 312..1787
FT CDS /*tag= a
XX
PN US5550023-A.

XX
27-AUG-1996.
PD
XX
18-MAY-1994; 94US-0024550.
XX
07-APR-1992; 92US-00867810.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
PA (UWJO) UNIV JOHNS HOPKINS.
PT Vogelstein B, Kinzler KW;
XX
DR WPI; 1996-401591/40.
P-PSDB; AAW07887.
XX
PT Identification of cpds. interfering with human MDM2/p53 binding - useful
as therapeutic agents to treat human neoplastic cells.
XX
PS Example 1; Col 21-26; 36pp; English.
XX
AAT45151 is a cDNA clone of the human MDM-2 gene derived from a human
colon carcinoma cell line Caco-2. The MDM-2 protein produced by this
clone is used in a method for identifying compounds that interfere with
the binding of p53 and MDM-2. In binding the p53 protein, the MDM-2
protein releases a cell from p53-regulated growth, allowing cancers to
develop. Therefore compounds identified as interfering with the binding
of MDM-2 to p53 are potentially useful in the treatment of human
neoplastic cells. In the method pref. one or both of the proteins is a
fusion protein esp. with an antibody or antibody fragment which aids
separation and identification. (updated on 25-MAR-2003 to correct PP
field.)
XX
Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

Query Match 100.0%; Score 402; DB 2; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3e-106; Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ATGNGCAATTCACAGATGTGTACTACTGATGGTGTGTAACCACTTCACAGATTCA 60
Db 312 ATGTCGAATTCACAGATGTGTACTACTGATGGTGTGTAACCACTTCACAGATTCA 371
Oy 61 GCTTCGGAAAGAGACCTGGTGTGACCAAGAACGATGCTTGTGAAGTATTAAGCT 120
Db 372 GCTTCGGAAAGAGACCTGGTGTGACCAAGAACGATGCTTGTGAAGTATTAAGCT 431
Oy 121 GTGCGTGACAAAGACACTTACTATGAGAGGTCTTTTACTGGCCAGAT 180
Db 432 GTGCGTGACAAAGACACTTACTATGAGAGGTCTTTTACTGGCCAGAT 491
Oy 181 ATTAGACTAAACGATTATATGAGAGAACACATAATGTTATATGGTCATGAT 240
Db 492 ATTAGACTAAACGATTATATGAGAGAACACATAATGTTATATGGTCATGAT 551
Oy 241 CTCTAGGAGATTGTTGGGTGCGTCAAGCTTCCTGTGAAAGGACAGGAAATAT 300
Db 552 CTCTAGGAGATTGTTGGGTGCGTCAAGCTTCCTGTGAAAGGACAGGAAATAT 611
Oy 301 ACCATGATCTACAGAACTTGTAGTGTAACTAGCAGGAACTCGGACTCGGTCA 360
Db 612 ACCATGATCTACAGAACTTGTAGTGTAACTAGCAGGAACTCGGACTCGGTCA 671
Oy 361 TCTGAGTGAGAACAGGTGCACTTGAGGTTGGAGTAT 402
Db 672 TCTGAGTGAGAACAGGTGCACTTGAGGTTGGAGTAT 713

RESULT 13
AAT66410
ID AAT66410 standard; cDNA; 2372 BP.
XX
AC AAT66410;

XX
DT 25-MAR-2003 (revised)
DT 14-SEP-2000 (revised)
DT 18-JUN-1997 (first entry)
XX
DE Human MDM2 coding sequence.
KW Human; MDM2 protein; antibody; detection; cancer; diagnosis;
KW p53-regulated growth; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS ID 312..1787
FT /*tag= a
FT /product= "MDM2"
XX
PN US5618921-A.
XX
PD 08-APR-1997.
XX
PP 17-FEB-1995; 95US-00390479.
XX
PR 07-APR-1992; 92US-00867840.
PR 23-JUN-1992; 92US-00903103.
PR 07-APR-1993; 93US-00044619.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI vogelstein B, Kinzler KW, Burrell M, Hill DE;
XX
DR WPI; 1997-225474/20.
XX
DR P-PSDB; AAW15463.
XX
PT Antibodies specific for human MDM2 protein - for diagnosis of cancer.
XX
PS Claim 1; Col 19-24; 35pp; English.
CC This sequence encodes the human MDM2 protein. Antibodies that
specifically bind to human MDM2 protein may be used for detecting
elevated expression of the MDM2 gene in a human tissue or body fluid
sample, esp. for cancer diagnosis. The antibodies may be used to
interfere with the binding of p53 to MDM2. Elevated levels of MDM2 appear
to sequester p53 and allow the cell to escape from p53-regulated growth.
(N.B. Revised record issued to correct the sequence analysis field.)
(Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
Best Local Similarity 100.0%; Score 402; DB 2; Length 2372;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ov 1 ATGTCGAATCCAACATGTCGTGACTCATGGTGTCTTAACCACTTCACAGATTCCA 60
Db 312 ATGTCGAATCCAACATGTCGTGACTCATGGTGTCTTAACCACTTCACAGATTCCA 371
Ov 61 GCTTCGAAAGAGACGCCCTGGTAGACCAGAACGCCCTGGTGAAGAGGACAGAA 120
Db 372 GCTTCGAAAGAGACGCCCTGGTAGACCAGAACGCCCTGGTGAAGAGGACAGAA 431
XX
PS Claim 1; Col 21-24; 35pp; English.
CC The present sequence is the human MDM2 cDNA, which was isolated from a
human Caco-2 colonic carcinoma cell cDNA library using a murine MDM2 cDNA
probe. The MDM2 cDNA can be used as a probe to detect the amplification
or elevated expression of a human MDM2 gene, which is diagnostic of
neoplasia or the potential for neoplastic transformation, useful for the
detection of, e.g. carcinomas, colorectal carcinoma, lung cancer and
chronic myelogenous leukaemia. (Updated on 25-MAR-2003 to correct PF
field.)
XX
SQ Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
Best Local Similarity 100.0%; Score 402; DB 2; Length 2372;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ov 1 ATGTCGAATCCAACATGTCGTGACTCATGGTGTCTTAACCACTTCACAGATTCCA 60
Db 312 ATGTCGAATCCAACATGTCGTGACTCATGGTGTCTTAACCACTTCACAGATTCCA 371
Ov 492 ATTATGACTAACAGATATTATGATGAGAACACATATTGTATTTCTGGCGAT 551
Db 432 GTGGGTGCAACAAAGACATTTATGATGAGAACACATATTGTATTTCTGGCGAT 491
Ov 181 ATTATGACTAACAGATATTATGATGAGAACACATATTGTATTTCTGGCGAT 240
Db 421 CTCTCTAGGAGATTGTGCGTCCAGCTCTCTGTGAAAGAGCACAGAAATAT 300
Db 552 CTCTCTAGGAGATTGTGCGTCCAGCTCTCTGTGAAAGAGCACAGAAATAT 611
XX
PS Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;
Best Local Similarity 100.0%; Score 402; DB 2; Length 2372;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Ov 1 ATGTCGAATCCAACATGTCGTGACTCATGGTGTCTTAACCACTTCACAGATTCCA 60
Db 312 ATGTCGAATCCAACATGTCGTGACTCATGGTGTCTTAACCACTTCACAGATTCCA 371
Ov 61 GCTTCGAAAGAGACGCCCTGGTAGACCAGAACGCCCTGGTGAAGAGGACAGAA 120

Query Match 100.0%; Score 402; DB 2; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 3e-106;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 372 GCTTCGAACTAGAGACCTGGTAGACCAAGCATTGGTTAGTTAGTTAAGTC; 431
 Qy 121 GTTGGGCAAAAGACACTATATATAGAAGGGTTTTATCTGGCAGAT 180
 Db 432 GTTGGGCAAAAGACACTATATAGAAGGGTTTTATCTGGCAGAT 491
 Qy 181 ATTACTAAACGATATAATGAGAGAACACATTTGATATGTCAGAT 240
 Db 492 ATTACTAAACGATATAATGAGAGAACACATTTGTCAGAT 551
 Qy 241 CTCTAGGAGATTGGTGGCGCAAGCTCTGTAGAACAGACAGAAATAT 300
 Db 552 CTCTAGGAGATTGGTGGCGCAAGCTCTGTAGAACAGACAGAAATAT 611
 Qy 301 ACCATGATCTACAGAACCTGTTAGACAAACCCATGCTTGAGTTAAGCT 360
 Db 612 ACCATGATCTACAGAACCTGTTAGACAAACCCATGCTTGAGTTAAGCT 671
 Db 672 TCTGTGAGTGAACAGGTCTACCTTGAGGTGGAGTCAT 713
 Qy 361 TCTGTGAGTGAACAGGTCTACCTTGAGGTGGAGTCAT 402
 Db 492 ATTACTAAACGATATAATGAGAGAACACATTTGTCAGAT 551
 Qy 241 CTCTAGGAGATTGGTGGCGCAAGCTCTGTAGAACAGACAGAAATAT 300
 Db 552 CTCTAGGAGATTGGTGGCGCAAGCTCTGTAGAACAGACAGAAATAT 611
 Qy 301 ACCATGATCTACAGAACCTGTTAGACAAACCCATGCTTGAGTTAAGCT 360
 Db 612 ACCATGATCTACAGAACCTGTTAGACAAACCCATGCTTGAGTTAAGCT 671
 Qy 361 TCTGTGAGTGAACAGGTCTACCTTGAGGTGGAGTCAT 402
 Db 672 TCTGTGAGTGAACAGGTCTACCTTGAGGTGGAGTCAT 713

RESULT 15

AAV20549

ID AAV20549 standard; cDNA; 2372 BP.

XX

AC AAV20549;

XX

DT 18-JUN-1998 (first entry)

XX

DE Human MDM2 encoding cDNA.

XX

KW Human; MDM2; hMDM2; tumour; cancer; diagnosis; neoplastic disease; barcoma; liposarcoma; malignant fibrous histiocytoma; osteosarcoma; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 312..1787

FT /tag= a

FT /product= "MDM2"

XX

PN US5736338-A.

XX

PD 07-APR-1998.

XX

PP 17-FEB-1995; 95US-00390517.

XX

PR 07-APR-1992; 92US-00867840.

PR 23-JUN-1992; 92US-00903103.

PR 07-APR-1993; 93US-00044619.

XX

PA (DJO) UNIV JOHNS HOPKINS.

XX

PT Vogelstein B, Kinzler KW, Hill DE, Burrell M;

XX

DR WPT; 1998-239206/21.

DR P-PSDB; PAW49241.

XX

Cancer diagnosis - by determination of MDM2 protein.

XX

Claim 1; Col 21-24; 35pp; English.

XX

CC The present sequence encodes human MDM2 (hMDM2) which is used in the method of the present invention. The present invention describes a method for diagnosing a neoplastic disease caused by overexpression of MDM2 protein. The method comprises detecting an elevated cellular amount of this protein. The method is useful for the diagnosis of sarcoma, especially liposarcoma, malignant fibrous histiocytoma or osteosarcoma.

XX

Sequence 2372 BP; 698 A; 491 C; 541 G; 642 T; 0 U; 0 Other;

SQ

Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6			
Run on:	October 18, 2004, 11:45:45 ; Search time 374 Seconds			
Scoring table:	IDENTITY_NUC			
Gapop	10.0 , Gapext 1.0			
Searched:	824507 seqs, 35539441 residues			
Total number of hits satisfying chosen parameters:	1649014			
Minimum DB seq length:	0			
Maximum DB seq length:	200000000			
Post-processing:	Minimum Match 0% Listing first 45 summaries			
Database :	Issued_Patents_NA:*			
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	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.			
	SUMMARIS			
Result No.	Score	Query Length	DB ID	Description
1	402	100.0	652	3 US-09-510-252-3
2	402	100.0	729	4 US-09-510-252-3
3	402	100.0	2372	1 US-07-903-103-1
4	402	100.0	2372	1 US-08-044-619A-1
5	402	100.0	2372	1 US-08-283-911-1
6	402	100.0	2372	1 US-08-245-500A-2
7	402	100.0	2372	1 US-08-390-546A-2
8	402	100.0	2372	1 US-08-390-479A-2
9	402	100.0	2372	1 US-08-557-393-2
10	402	100.0	2372	1 US-08-390-516C-2
11	402	100.0	2372	1 US-08-073-517A-2
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14	402	100.0	2372	3 US-09-073-567-1
15	402	100.0	2372	3 US-09-280-805-1
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17	402	100.0	2372	3 US-09-170-159A-2
18	402	100.0	2372	4 US-09-480-718-43
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20	289.2	71.9	1710	1 US-08-044-619A-3
21	289.2	71.9	1710	1 US-08-283-911-3
22	289.2	71.9	1710	1 US-08-245-500A-4
23	289.2	71.9	1710	1 US-08-390-546-4
24	289.2	71.9	1710	1 US-08-390-479A-4
25	289.2	71.9	1710	1 US-08-557-393-4
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27	289.2	71.9	1710	1 US-08-390-517A-4
				RESULT 1
				; Sequence 3, Application US/09510252
				; Patent No. 637290
				; GENERAL INFORMATION:
				; APPLICANT: Nandabalan, Krishnan
				; APPLICANT: Yang, Meijia
				; APPLICANT: Schulz, Vincent
				; APPLICANT: Curagen Corporation
				; TITLE OF INVENTION: MDM INTERACTING PROTEIN AND METHODS OF USE THEREOF
				; FILE REFERENCE: 1966-524 MDM US
				; CURRENT APPLICATION NUMBER: US/09/510,252
				; CURRENT FILING DATE: 2000-02-22
				; PRIOR APPLICATION NUMBER: USSN 6/121,192
				; PRIOR FILING DATE: 1999-02-23
				; PRIOR APPLICATION NUMBER: USSN 6/0122,643
				; PRIOR FILING DATE: 1999-03-03
				; NUMBER OF SEQ ID NOS: 4
				; SOFTWARE: Patentin Ver. 2.0
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				; LENGTH: 652
				; TYPE: DNA
				; ORGANISM: Homo sapiens
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				Query Match 100%; Score 402; DB 3; Length 652;
				Best Local Similarity 100.0%; Prcd. No. 2; Je-103; 0; Mismatches 0; Indels 0; Gaps 0;
				Matches 402; Conservative 1.
			QY	1 ATGGCAATACCAACATGTCTGACCTACTGTAGTGTGCTGTAACCAACCTCACAGATTCA 60
				1 ATGGCAATACCAACATGTCTGACCTACTGTAGTGTGCTGTAACCAACCTCACAGATTCA 60
			QY	61 GCTTGGACAGAGACCTGTAGCAACGCCATTCTTGATGAGAGGTCTTTATCTTGCGCAT 120
				61 GCTTGGACAGAGACCCGTGTTAGACCAAAGCCATTCTTGATGAGAGGTCTTTATCTTGCGCAT 120
			QY	181 ATTAGCTAACGATTATATGAGAAGACAAACATATGATATGTCAATGAT 240
				181 ATTAGCTAACGATTATATGAGAAGACAAACATATGATATGTCAATGAT 240
			QY	121 GTTGGTGCACAAAGACACTTACTATGAGAGGTCTTTATCTTGCGCAT 180
				121 GTTGGTGCACAAAGACACTTACTATGAGAGGTCTTTATCTTGCGCAT 180
			QY	241 CTCTCTAGGAGATGTTGCGTGCACAGCTCTGTGAAAGAGCCAGGAAATAT 300
				241 CTCTCTAGGAGATGTTGCGTGCACAGCTCTGTGAAAGAGCCAGGAAATAT 300
			QY	301 ACCATGATCTACAGGAACTTGGTAGTCAATCAGCAGGAATCATCGCACTCAGGTACA 360

RESULT 2
 US-09-603-052-3
 Sequence 3, Application US/09603052
 Patent No. 649216

GENERAL INFORMATION:
 APPLICANT: Chene, Patrick
 APPLICANT: Hockeppel, Heinz-Kurt
 TITLE OF INVENTION: Assay for identifying inhibitors of the interaction
 TITLE OF INVENTION: Between proteins p53 and dm2
 FILE REFERENCE: MEWB6.001C1

CURRENT APPLICATION NUMBER: US/09/603, 052
 CURRENT FILING DATE: 2000-06-26
 PRIOR APPLICATION NUMBER: EP 95810576.9
 PRIOR FILING DATE: 1995-09-18
 PRIOR APPLICATION NUMBER: PCT/EP96/03957
 PRIOR FILING DATE: 1996-03-10

NUMBER OF SEQ ID NOS: 11
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 729

TYPE: DNA
 ORGANISM: Homo sapiens

FEATURE:
 NAME/KEY: CDS
 LOCATION: (84)..(650)

OTHER INFORMATION: N-terminal 188 amino acids of human double minute
 US-09-603-052-3

Query Match 100.0%; Score 402; DB 4; Length 729;
 Best Local Similarity 100.0%; Pred. No. 2, 4e-103; Gaps 0;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCGAATCCACATGTTGTAATGATGGTGTCAACCACTCACAGATCCA 60
 QY 61 GCTTCGGAAAGAGAGACCTGTTAGACCAAGGCATGCTTTGAAGTTAAAGCT 120
 QY 144 GCTTGGAAACAGAGACCTGTTAGACCAAGGCATGCTTTGAAGTTAAAGCT 203
 QY 121 GTTGGTGACACAAAGACACTTATCTGAAAGGGTTTTTATCTGCCAGAT 143
 QY 84 ATGTCGAATCCACATGTTGTAATGATGGTGTCAACCACTCACAGATCCA 143
 Db 84 ATGTCGAATCCACATGTTGTAATGATGGTGTCAACCACTCACAGATCCA 143
 Db 61 GCTTCGGAAAGAGAGACCTGTTAGACCAAGGCATGCTTTGAAGTTAAAGCT 120
 Db 144 GCTTGGAAACAGAGACCTGTTAGACCAAGGCATGCTTTGAAGTTAAAGCT 203
 QY 181 ATTAGCACTAACGTTATGATGAGACACATATGATATGTCATATGAT 240
 Db 264 ATTAGCACTAACGTTATGATGAGACACATATGTCATATGAT 323
 Db 204 GTTGGTGACACAAAGACACTTATCTGAAAGGGTTTTTATCTGCCAGAT 263
 QY 181 ATTAGCACTAACGTTATGATGAGACACATATGATATGTCATATGAT 240
 Db 264 ATTAGCACTAACGTTATGATGAGACACATATGTCATATGAT 323
 Db 204 GTTGGTGACACAAAGACACTTATCTGAAAGGGTTTTTATCTGCCAGAT 263
 QY 241 CTCCTAGGAGATTGTTGGGTGCAAGGTTCCTGTGAAAGAGCACAGAAATAT 300
 Db 324 CTCTAGGAGATTGTTGGGTGCAAGGTTCCTGTGAAAGAGCACAGAAATAT 383
 QY 301 ACCATGATCTACAGAACTGGTAGTGTCAATCGAGGAATCATCGACTAGTACA 360
 Db 384 ACCATGATCTACAGAACTGGTAGTGTCAATCGAGGAATCATCGACTAGTACA 443
 QY 361 TCTGAGTGTAGACAGGGTCACCTGGAGGTGGAGT 402
 Db 444 TCTGAGTGTAGACAGGGTCACCTGGAGGTGGAGT 485

Query Match 100.0%; Score 402; DB 1; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 3, 5e-103; Gaps 0;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCGAATCCACATGTTGTAATGATGGTGTCAACCACTCACAGATCCA 60
 Db 312 ATGTCGAATCCACATGTTGTAATGATGGTGTCAACCACTCACAGATCCA 371
 QY 61 GCTTCGGAAAGAGAGACCTGTTAGACCAAGGCATGCTTTGAAGTTAAAGCT 120
 Db 372 GCTTCGGAAAGAGAGACCTGTTAGACCAAGGCATGCTTTGAAGTTAAAGCT 431
 QY 121 GTTGGTGACACAAAGACACTTATGATGAGACACATATGTCATATGAT 180
 Db 432 GTTGGTGACACAAAGACACTTATGATGAGACACATATGTCATATGAT 491
 QY 181 ATTAGCACTAACGTTATGATGAGACACATATGTCATATGTCATATGAT 240
 Db 492 ATTAGCACTAACGTTATGATGAGACACATATGTCATATGTCATATGAT 551

RESULT 3
 US-07-903-103-1
 Sequence 1, Application US/07903103

RESULT 4

US-08-044-619A-1

; Sequence 1, Application US/08044619A

; Patent No. 5420263

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY

APPLICATION: 720 RUTLIAND AVENUE, BALTIMORE, MARYLAND 21205 USA

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN

TITLE OF INVENTION: HUMAN TUMORS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT

STREET: 1001 G ST., N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/044,619A

FILING DATE: 07-APR-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/903,103

FILING DATE: 23-JUN-1992

APPLICATION NUMBER: US 07/867,840

FILING DATE: 07-APR-1992

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.40148

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2372 base pairs

TYPE: nucleic acid

STRANDNESS: double

TOPOLOGY: linear

MOLCULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

CELL LINE: Caco-2

POSITION IN GENOME:

MAP POSITION: 12q12-14

FEATURE:

NAME/KEY: CDS

LOCATION: 312..1784

US-08-044-619A-1

Query Match Local Similarity 100.0%; Score 402; DB 1; Length 2372;

Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

US-08-283-911-1

; Sequence 1, Application US/08283911

; Patent No. 5519118

GENERAL INFORMATION:

APPLICANT: VOGELSTEIN, BERT

APPLICATION: KINZLER, KENNETH

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN

TITLE OF INVENTION: HUMAN TUMORS

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT

STREET: 1001 G ST., N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/283,911

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/903,103

FILING DATE: 23-JUN-1992

APPLICATION NUMBER: US 07/867,840

FILING DATE: 07-APR-1992

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.40148

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2372 base pairs

Qry 241 CTTCTAGGAGATTGTTGGGGTGCACAGCTCTCTGTGAAAGGACAGGAATATAT 300

Db 552 CTTCTAGGAGATTGTTGGGGTGCACAGCTCTCTGTGAAAGGACAGGAATATAT 611

Qry 301 ACCATGATCAGGACTTGTGAGTGTAGTATCAGCAGGATCATCGGATCTCGTAC 360

Db 612 ACCATGATCAGGACTTGTGAGTGTAGTATCAGCAGGATCATCGGATCTCGTAC 671

Qry 361 TCTGAGTGGAGAACGGTGTACCTGAGGTGGAGTGT 402

Db 672 TCTGAGTGGAGAACGGTGTACCTGAGGTGGAGTGT 713

Qry 432 GTTGGGCAACAAAGACACTATACATGAAAGGGTCTTTTATCTGGCGAT 491

Qry 181 ATTATGACTAACGATATATGATGAGAAGCAGAACATATTGATATGTTCAAATGAT 240

Db 492 ATTATGACTAACGATATATGATGAGAAGCAGAACATATTGATATGTTCAAATGAT 551

Qry 241 CTTCTAGGAGATTGTTGGGGTGCACAGCTCTCTGTGAAAGGACAGGAATATAT 300

Db 552 CTTCTAGGAGATTGTTGGGGTGCACAGCTCTCTGTGAAAGGACAGGAATATAT 611

Qry 301 ACCATGATCAGGACTTGTGAGTGTAGTATCAGCAGGATCATCGGATCTCGTAC 360

Db 612 ACCATGATCAGGACTTGTGAGTGTAGTATCAGCAGGATCATCGGATCTCGTAC 671

Qry 361 TCTGAGTGGAGAACGGTGTACCTGAGGTGGAGTGT 402

Db 672 TCTGAGTGGAGAACGGTGTACCTGAGGTGGAGTGT 713

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-283-911-1

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3..5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTCATAATCCAAACATGTTGACTACTGATGGTGTGTTAACCAACCTCACAGATTCA 60
Db 312 ATGTCATAATCCAAACATGTTGACTACTGATGGTGTGTTAACCAACCTCACAGATTCA 371
Qy 61 GCTTCGGAAAGAGACCCCTGGTTAGACCAAGGCATTTGAAAGTTAAAGCT 120
Db 372 GCTTCGGAAAGAGACCCCTGGTTAGACCAAGGCATTTGAAAGTTAAAGCT 431
Qy 121 GTGGGTGACAAAGAGACCTTACATGAAAGAGGTCTTTTATCTGGCCAGAT 180
Db 432 GTTGGTGACAAAGAGACCTTACATGAAAGAGGTCTTTTATCTGGCCAGAT 491
Qy 181 ATATGACTAAACGATTATGATGAGAACACAAACATATGTTATGTTCAATGAT 240
Db 492 ATATGACTAAACGATTATGATGAGAACACAAACATATGTTATGTTCAATGAT 551
Qy 241 CTCTTAGGAGATTGTTGGCGTSCCAACCTTCCTGTGAAGAGACAGGAATAAT 300
Db 552 CTCTTAGGAGATTGTTGGCGTSCCAACCTTCCTGTGAAGAGACAGGAATAAT 611
Qy 301 ACCATGATCTACAGGAACCTGGTAGTAGTCAATCGCAGGAATCATCGGACTCAGGTA 360
Db 612 ACCATGATCTACAGGAACCTGGTAGTAGTCAATCGCAGGAATCATCGGACTCAGGTA 671
Db 361 TCTGTGAGTGAACAGGTGTCACCTGAAGGTGGAGTAT 402
Qy 672 TCTGTGAGTGAACAGGTGTCACCTGAAGGTGGAGTAT 713

RESULT 6
US-08-245-500A-2
; Sequence 2, Application US/08245500A
; Patent No. 550023
; GENERAL INFORMATION:
; APPLICANT: BURREL, MARILEE
; BURREL, MARILEE
; HILL, DAVID E.
; KINZLER, KENNETH W.
; VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; TITLE OF INVENTION: HUMAN TUMORS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,500A
FILING DATE: 07-APR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42798
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9289
TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL LINE: Caco-2
POSITION IN GENOME:
MAP POSITION: 12q12-14
FEATURE:
NAME/KEY: CDS
LOCATION: 312..1784
US-08-245-500A-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
Best Local Similarity 100.0%; Pred. No. 3..5e-103;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTCATAATCCAAACATGTTGACTACTGATGGTGTGTTAACCAACCTCACAGATTCA 60
Db 312 ATGTCATAATCCAAACATGTTGACTACTGATGGTGTGTTAACCAACCTCACAGATTCA 371
Qy 61 GCTTCGGAAAGAGACCCCTGGTTAGACCAAGGCATTTGAAAGTTAAAGCT 120
Db 372 GCTTCGGAAAGAGACCCCTGGTTAGACCAAGGCATTTGAAAGTTAAAGCT 431
Qy 121 GTGGGTGACAAAGAGACCTTACATGAAAGAGGTCTTTTATCTGGCCAGAT 180
Db 432 GTTGGTGACAAAGAGACCTTACATGAAAGAGGTCTTTTATCTGGCCAGAT 491
Qy 181 ATATGACTAAACGATTATGATGAGAACACAAACATATGTTATGTTCAATGAT 240
Db 492 ATATGACTAAACGATTATGATGAGAACACAAACATATGTTATGTTCAATGAT 551
Qy 241 CTCTTAGGAGATTGTTGGCGTSCCAACCTTCCTGTGAAGAGACAGGAATAAT 300
Db 552 CTCTTAGGAGATTGTTGGCGTSCCAACCTTCCTGTGAAGAGACAGGAATAAT 611
Qy 301 ACCATGATCTACAGGAACCTGGTAGTAGTCAATCGCAGGAATCATCGGACTCAGGTA 360
Db 612 ACCATGATCTACAGGAACCTGGTAGTAGTCAATCGCAGGAATCATCGGACTCAGGTA 671
Qy 361 TCTGTGAGTGAACAGGTGTCACCTGAAGGTGGAGTAT 402
Db 672 TCTGTGAGTGAACAGGTGTCACCTGAAGGTGGAGTAT 713

RESULT 7
US-08-30-546-2
; Sequence 2, Application US/0830546
; Patent No. 5605046
; GENERAL INFORMATION:
; APPLICANT: BURREL, MARILEE
; BURREL, MARILEE
; HILL, DAVID E.
; KINZLER, KENNETH W.
; VOGELSTEIN, BERT

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 TITLE OF INVENTION: HUMAN TUMORS
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
 STREET: 1001 G STREET, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20001
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/390,546
 FILING DATE: 07-APR-1993
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: KAGAN, SARAH A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 01107.42798
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9100
 TELEFAX: 202-508-9299
 TELEX: 197430 BMB-UT
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2372 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 CELL LINE: CaCo-2
 POSITION IN GENOME:
 MAP POSITION: 12q12-14
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 312..1784
 ;
 ; US-08-390-546-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 3..5e-103; Length 2372;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCGAATCCAACTAGTGTGACTTACTGATGGCTGCTTAACACCTCACAGATTCA 60
 Db 312 ATGTGCAATACCAACATGTCTGACTACTATGGCTGCTTAACACCTCACAGATTCA 371
 Qy 61 GCTTCGAGACAGAGACCCCTGGTAGACCAAGGCAATTGCTTGGTAAAGCT 120
 Db 372 GCTTCGGAACAGAGACCCCTGGTAGACCAAGGCAATTGCTTGGTAAAGCT 431
 Qy 121 GTGGGTGACAAAGAGACACTATACATGAAAGAGGTCTTTTATCTGGCAAGTAT 180
 Db 432 GTGGGTGACAAAGAGACATATACATGAAAGAGGTCTTTTATCTGGCAAGTAT 491
 Qy 181 ATTATGACTAACGATTATGTGAGGAGAACACATATGTATATGTCAATGAT 240
 Db 492 ATTATGACTAACGATTATGTGAGGAGAACACATATGTATATGTCAATGAT 551
 Qy 241 CTCTCAGGAGATTGTTGGCTGCGAGCTCTGTGAAAGACAGCAAGGAATATAT 300
 Db 552 CTTCAGGAGATTGTTGGCTGCGAGCTCTGTGAAAGACAGCAAGGAATATAT 611
 Qy 301 ACCATGATCTAACGAGACTGGTAGTAGTAACTAGCAGGAAATCTGGCACTAGTCA 360
 Db 612 ACCATGATCTAACGAGACTGGTAGTAGTAACTAGCAGGAAATCTGGCACTAGTCA 671

RESULT 8
 US-08-390-479A-2
 ; Sequence 2, Application US/08390479A
 ; Patent No. 5618921
 ; GENERAL INFORMATION:
 ; APPLICANT: BURRELL, MARILEE
 ; APPLICANT: HILL, DAVID E.
 ; APPLICANT: KINZLER, KENNETH W.
 ; APPLICANT: VOGELSTEIN, BERT
 ; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
 ; TITLE OF INVENTION: HUMAN TUMORS
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BANNER & WITCOFF, LTD.
 ; STREET: 1001 G STREET, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20001
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/390,479A
 FILING DATE: 02-FEB-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: KAGAN, SARAH A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 01107.48992
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9100
 TELEFAX: 202-508-9299
 TELEX: 197430 BMB-UT
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2372 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 CELL LINE: CaCo-2
 POSITION IN GENOME:
 MAP POSITION: 12q12-14
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 312..1784
 ;
 ; US-08-390-479A-2

Query Match 100.0%; Score 402; DB 1; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 3..5e-103; Length 2372;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCGAATCCAACTAGTGTGACTTACTGATGGCTGCTTAACACCTCACAGATTCA 60
 Db 312 ATGTGCAATACCAACATGTCTGACTACTATGGCTGCTTAACACCTCACAGATTCA 371
 Qy 61 GCTTCGAGACAGAGACCCCTGGTAGACCAAGGCAATTGCTTGGTAAAGCT 120
 Db 372 GCTTCGGAACAGAGACCCCTGGTAGACCAAGGCAATTGCTTGGTAAAGCT 431
 Qy 61 GCTTCGAGACAGAGACCCCTGGTAGACCAAGGCAATTGCTTGGTAAAGCT 402
 Db 372 GCTTCGAGACAGAGACCCCTGGTAGACCAAGGCAATTGCTTGGTAAAGCT 713

RESULT 9

US-08-557-393-2

; Sequence 2, Application US/08557393

; GENERAL INFORMATION:

; APPLICANT: BURRELL, MARILLE

; APPLICANT: HILL, DAVID E.

; APPLICANT: KINZLER, KENNETH W.

; APPLICANT: VOGELSTEIN, BERT

; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN HUMAN TUMORS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT

STREET: 1001 G STREET, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/557,393

FILING DATE: 13-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/245,500

FILING DATE: 18-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.42798

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 197430 BMB UT

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2372 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORGANISM: Homo sapiens

CELL LINE: Caco-2

POSITION IN GENOME:

RESULT 10

US-08-90-516C-2

; Sequence 2, Application US/08390516C

; Patent No. 5708136

; GENERAL INFORMATION:

; APPLICANT: BURRELL, MARILLE

; APPLICANT: HILL, DAVID E.

; APPLICANT: KINZLER, KENNETH W.

; APPLICANT: VOGELSTEIN, BERT

; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN HUMAN TUMORS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT

STREET: 1001 G STREET, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/390,516C

FILING DATE: 07-APR-1993

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.42798

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

GENERAL INFORMATION:

APPLICANT: BURRELL, MARILEE

APPLICANT: HILL, DAVID E.

APPLICANT: KINZLER, KENNETH W.

APPLICANT: VOGELSTEIN, BERT

TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT

STREET: 1001 G STREET, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/390,515A

FILING DATE: 07-APR-1993

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.

REGISTRATION NUMBER: 32.141

REFERENCE/DOCKET NUMBER: 01107.42798

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100

TELEFAX: 202-508-9299

TELEX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2372 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

CELL LINE: Caco-2

POSITION IN GENOME:

MAP POSITION: 12q12-14

FEATURE:

NAME/KEY: CDS

LOCATION: 312..1784

; US-08-390-515A-2

Query Match Similarity 100.0%; Score 402; DB 1; Length 2372; Best Local Similarity 100.0%; Pred. No. 3.5e-103; Mismatches 402; Conservative 0; MisMatches 0; Indels 0; Gaps 0; Matches 402; ;

Query Match Similarity 100.0%; Score 402; DB 1; Length 2372; Best Local Similarity 100.0%; Pred. No. 3.5e-103; Mismatches 402; Conservative 0; MisMatches 0; Indels 0; Gaps 0; Matches 402; ;

Query Match Similarity 100.0%; Score 402; DB 1; Length 2372; Best Local Similarity 100.0%; Pred. No. 3.5e-103; Mismatches 402; Conservative 0; MisMatches 0; Indels 0; Gaps 0; Matches 402; ;

Query Match Similarity 100.0%; Score 402; DB 1; Length 2372; Best Local Similarity 100.0%; Pred. No. 3.5e-103; Mismatches 402; Conservative 0; MisMatches 0; Indels 0; Gaps 0; Matches 402; ;

Query Match Similarity 100.0%; Score 402; DB 1; Length 2372; Best Local Similarity 100.0%; Pred. No. 3.5e-103; Mismatches 402; Conservative 0; MisMatches 0; Indels 0; Gaps 0; Matches 402; ;

Query Match Similarity 100.0%; Score 402; DB 1; Length 2372; Best Local Similarity 100.0%; Pred. No. 3.5e-103; Mismatches 402; Conservative 0; MisMatches 0; Indels 0; Gaps 0; Matches 402; ;

Query Match Similarity 100.0%; Score 402; DB 1; Length 2372; Best Local Similarity 100.0%; Pred. No. 3.5e-103; Mismatches 402; Conservative 0; MisMatches 0; Indels 0; Gaps 0; Matches 402; ;

RESULT 13
US-08-801-718-2
Sequence 2, Application US/08801718
; Patient No. 5858976
; GENERAL INFORMATION:
; APPLICANT: BURRELL, MARILEE
; APPLICANT: HILL, DAVID E.
; APPLICANT: KINZLER, KENNETH W.
; APPLICANT: VOGELSTEIN, BERT
; TITLE OF INVENTION: AMPLIFICATION OF HUMAN MDM2 GENE IN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
; STREET: 1001 G STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/801,718
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/390,515
FILING DATE: 07-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32.141
REFERENCE/DOCKET NUMBER: 01107.42798

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 197430 BBMB UT

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2372 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

CELL LINE: Caco-2

POSITION IN GENOME:

MAP POSITION: 12q12-14

FEATURE:

NAME/KEY: CDS

LOCATION: 312..1784

; US-08-801-718-2

Query Match Similarity 100.0%; Score 402; DB 2; Length 2372; Best Local Similarity 100.0%; Pred. No. 3.5e-103; Mismatches 402; Conservative 0; MisMatches 0; Indels 0; Gaps 0; Matches 402; ;

Query Match 100.0%; Score 402; DB 3; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 3.5e-103;
 Matches. 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCGAAATCCACATGCTGTTACCTGATGGCTGTACCACTCACAGATCCA 60
 Db 312 ATGTCGAAATCCACATGCTGTTACCTGATGGCTGTACCACTCACAGATCCA 371

Qy 61 GCTTCGCAACAGAGAGCCCTGGTTAGACCAAGCCATGCTTTGAGTTAAGCT 120
 Db 372 GCTTCGCAACAGAGAGCCCTGGTTAGACCAAGCCATGCTTTGAGTTAAGCT 431

Qy 121 GTTGGTGCACAAAGAACACTATACATGAAAGAAGCTTCTTTATCTGGCCAGAT 180
 Db 492 ATTACTACAAAGCTTATGATGAGAAAGCAACACATTTGATATTGTCATGAT 551

Qy 241 CTCTCTAGGAAAGTTGTTGCGCTGCCAAGCTCTCTGTTGAAAGAGCACAGAAATAT 300
 Db 552 CTCTCTAGGAAAGTTGTTGCGCTGCCAAGCTCTCTGTTGAAAGAGCACAGAAATAT 611

Qy 301 ACCATGATCTACAGGACTTGTAGTGTAGAAAGCAACACATTTGATATTGTCATGAT 360
 Db 612 ACCATGATCTACAGGACTTGTAGTGTAGAAAGCAACACATTTGATATTGTCATGAT 671

Qy 361 TCTGTAAGTGAAGACAGGTGACCTTCACCTTGAAAGTGGAGTGT 402
 Db 672 TCTGTAAGTGAAGACAGGTGACCTTCACCTTGAAAGTGGAGTGT 713

RESULT 14

US-9-073-567-1 Application US/09073567
 Sequence 1, Application US/09073567
 Patent No. 6013786
 GENERAL INFORMATION:
 APPLICANT: Jiaodong Chen
 CORRESPONDENCE ADDRESS:
 STREET: 300 South Wacker Drive, 32nd Floor
 CITY: Chicago
 STATE: IL
 COUNTRY: United States of America
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/073,567
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Greenfield, Michael S.
 REGISTRATION NUMBER: 37,147
 REFERENCE/DOCKET NUMBER: 98, 057-A

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 913-0001
 TELEFAX: (312) 913-0002
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2372 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: hmdm2 DNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

US-9-073-567-1

RESULT 15

US-03-280-805-1 Application US/09280805
 Sequence 1, Application US/09280805
 Patent No. 618422
 GENERAL INFORMATION:
 APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
 APPLICANT: Graham, Brett P. Monia
 TITLE OF INVENTION: ANTI-SENSE MODULATION OF HUMAN MDM2
 NUMBER OF SEQUENCES: 271
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Law Offices of Jane Massey Licata
 STREET: 66 East Main Street
 CITY: Marion
 STATE: NJ
 COUNTRY: U.S.A.
 ZIP: 08053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 COMPUTER: IBM PC
 OPERATING SYSTEM: WINDOWS 95
 SOFTWARE: WORDPERFECT 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/280,805
 FILING DATE: herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/048,810
 FILING DATE: March 26, 1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Licata, Jane Massey
 REGISTRATION NUMBER: 32,257
 REFERENCE/DOCKET NUMBER: ISPH-0346
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 609-810-1515
 TELEFAX: 609-810-1454
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2372 base pairs
 TYPE: Nucleic Acid

STRANDEDNESS: Single
 TOPOLOGY: Unknown
 ANTI-SENSE: No
 PUBLICATION INFORMATION:
 AUTHORS: Oliner, J.D.
 AUTHORS: Kinzler, K.W.
 AUTHORS: Meltzer, P.S.
 AUTHORS: Vogelstein, B.
 TITLE: Amplification of a gene encoding a
 p53-associated protein in human sarcomas
 JOURNAL: Nature
 VOLUME: 358
 ISSUE: 6381
 PAGES: 80-83
 DATE: 02-JUL-1992
 US-09-280-805-1

Query Match 100.0%; Score 402; DB 3; Length 2372;
 Best Local Similarity 100.0%; Pred. No. 3.5e-103; Indels 0; Gaps 0;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGCCAATCCACAGATGCTGTACCTATGATGATGCTGTAACCACTCACAGATCCA 60
Db 312 ATGTCAAATACCAACATGTTGTAACCACTCACAGATCCA 371
Qy 61 GCTTCGGAAACAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAGTTATTAAGCT 120
Db 372 GCTTCGGAAACAGAGACCCCTGGTTAGACCAAGCCATTGCTTTGAGTTATTAAGCT 431
Qy 121 GTTGGTGCAACAAAGACCTTAACTATGAGAAAGGGTTTAACTTGCCAGTAT 180
Db 432 GTTGGTGCAACAAAGACCTTAACTATGAGAAAGGGTTTAACTTGCCAGTAT 491
Qy 181 ATTATGACTAACGATTATGATGAGAAACACATTTGATATGTTCAATGAT 240
Db 492 ATTATGACTAACGATTATGATGAGAAACACATTTGATATGTTCAATGAT 551
Qy 241 CTTCTAGGAGATTGTTGGCGTGCCAAAGTTCTGTGAGAAGAGCACGGAAATAT 300
Db 552 CTCTCTAGGAGATTGTTGGCGTGCCAAAGTTCTGTGAGAAGAGCACGGAAATAT 611
Qy 301 ACCATGATCTACAGGAACTTGTTGAGTAACTCAGAGAACTCGGAACTCAGGTACA 360
Db 612 ACCATGATCTACAGGAACTTGTTGAGTAACTCAGAGAACTCGGAACTCAGGTACA 671
Qy 361 TCTCTGAGTACAGGAACTTGTTGAGTAACTCAGAGAACTCGGAACTCAGGTACA 402
Db 672 TCTCTGAGTACAGGAACTTGTTGAGTAACTCAGAGAACTCGGAACTCAGGTACA 713

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Search completed: October 18, 2004, 14:58:20
 Job time : 377 secs

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Om nucleic - nucleic search, using sw model

Run on: October 18, 2004, 11:45:45 : Search time 7330 seconds (without alignments)

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_g881:*

9: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	402	100.0	970	4 BM479400 AGENCOURT
2	401	99.8	709	2 BM479400 AGENCOURT
3	394.6	98.2	739	7 CR629819
4	377.4	92.9	482	7 R80343
5	366.8	91.2	779	7 COT37650
6	365.8	91.2	858	7 COT37954
7	353	87.8	778	2 BE900427
8	347.6	80.5	778	7 COT38288
9	342.4	80.7	345	2 BE765314
10	324	80.6	393	1 AL7004062
11	318	79.1	518	1 A1902188
12	310	77.1	400	7 CNA49877
13	297.4	74.0	1008	2 BF683210
14	294.6	73.3	507	7 BF114786
15	294.6	73.3	512	2 BF435134
16	289.8	72.1	556	2 BP55339
17	289.8	72.1	774	7 CK469133
18	289.8	72.1	815	7 CK469134
19	289.8	72.1	822	7 CK588265
20	289.8	72.1	836	7 CK653033
21	289.8	72.1	845	7 CK470726
22	289.2	71.9	468	6 CD549480
23	289.2	71.9	468	6 CD562678
24	289.2	71.9	524	6 CA871480

Scoring table: IDENTITY_NUC Gapop 10-, Gapext 1.0

Searched: 32822875 seqb, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

ALIGNMENTS

RESULT	1
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LOCUS	BM479400 mRNA
DEFINITION	AGENCOURT 6418503 NIH_MGC_67
5', mRNA sequence.	
ACCESSION	BM479400
VERSION	BM479400.1
KEYWORDS	EST
SOURCE	Homo sapiens (human)
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1 (bases 1 to 970)
AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgbps-remail.nih.gov
FEATURES	Tissue procurement: ATCC
SOURCE	cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DATA	DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
Plate: LLM12140	row: f column: 01
High quality sequence stop: 597.	location/Qualifiers
1.	970
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="IMGR:552336"	
/tissue_type="retinoblastoma"	
/lab_host="DH10B (phage-resistant)"	
/clone_lid="NIH_MGC_67"	
/note="Organ: eye; Vector: PCMV-SP0R6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.75 kb. Library constructed by Life Technologies."	
ORIGIN	Query Match 100.0%; Score 402; DB 4; Length 970; Best Local Similarity 100.0%; Pred. No. 3; Te-101; Mismatches 402; Conservative 0; Indels 0; Gaps 0; OQY 1

went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match Similarity 99.8%; Score 401; DB 2; Length 709; Matches 401; Conservative 0; Pred. No. 6 5e-11; Mismatches 1; Indels 0; Gaps 0;

Db

1 ATGTCGAATACCAAGATGTGTGACTGATGCTGTTAACCACTACAGATTCA 135

61 GCTTGGAAAGAGACCTGGTTGAGCAGGCACTGCTTGAAGTTAAAGCT 120

136 GCTTGGAAAGAGACCTGGTTGAGCAGGCACTGCTTGAAGTTAAAGCT 195

121 GTTGGTCAQAAAGACACTTACTATGAAAGAGGTCCTTTATCTGGCAGAT 180

196 GTTGGTCAQAAAGACACTTACTATGAAAGAGGTCCTTTATCTGGCAGAT 255

181 ATTAGACTAACGATTATGATGAGAAGCAACATATTGATATGTCATATG 240

256 ATTAGACTAACGATTATGATGAGAAGCAACATATTGATATGTCATATG 315

241 CTCTTAGGAGATTGTTGGTGCACACTTCCTGTAAGAAGGACAGGAAATAT 300

316 CTCTTAGGAGATTGTTGGTGCACACTTCCTGTAAGAAGGACAGGAAATAT 375

301 ACCATGATCTACAGGAACTGGTAGTAGTCATCGAGGATCATGGCTCAGTACA 360

376 ACCATGATCTACAGGAACTGGTAGTAGTCATCGAGGATCATGGCTCAGTACA 435

361 TCTGTGAGTGAACAGGTGTCACCTGAAAGGTGGAGTAT 402

436 TCTGTGAGTGAACAGGTGTCACCTGAAAGGTGGAGTAT 477

RESULT 2

Db

301 ACCATGATCTACAGGAACTGGTAGTAGTCATCGAGGATCATGGCTCAGTACA 360

376 ACCATGATCTACAGGAACTGGTAGTAGTCATCGAGGATCATGGCTCAGTACA 435

386 ATTAGACTAACGATTATGATGAGAAGCAACATATTGATATGTCATATG 445

446 CTCTTAGGAGATTGTTGGTGCACACTTCCTGTAAGGAAATAT 505

301 ACCATGATCTACAGGAACTGGTAGTAGTCATCGAGGATCATGGCTCAGTACA 360

505 ACCATGATCTACAGGAACTGGTAGTAGTCATCGAGGATCATGGCTCAGTACA 565

361 TCTGTGAGTGAACAGGTGTCACCTGAAAGGTGGAGTAT 402

566 TCTGTGAGTGAACAGGTGTCACCTGAAAGGTGGAGTAT 607

ORIGIN

Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 709) NCI CGAP Ov18 Homo Sapiens cDNA clone IMAGE:3478285

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Geno Index

TITLE

Unpublished (1997)

VERSION

BR057574.1 GI:10811470

KEYWORDS

EST.

COMMENT

Contact: Robert Strauberg, Ph.D.

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL, send email to: info@image.lnl.gov

Seq primer: -40UP from Gibco

High quality sequence stop: 481.

FEATURES

source

1. -709

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="txaxon:9606"

/clone="IMAGE:3478285"

/tissue_type="fibrobloma"

/lab_host="M110B (phage-resistant)"

/clone_lib="NCI CGAP Ov18"

/note="Organ: ovary; Vector: pRT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TCTTACCATCGAGGGAGCGCGCCACATTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library

RESULT 3

Db

CR29819 CR629819 CR629819 CR629819 CR629819.1 GR:51125899

ORIGIN

Pongo pygmaeus (orangutan)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

REFERENCE

1 (bases 1 to 739) Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.

AUTHORS

Pongo pygmaeus mRNA (Bahr,A., Lauber,J., Mewes,H.W., et al.)

TITLE

Unpublished (2004)

JOURNAL

Contact: MIPS

COMMENT

Ingostaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp469A1622) is available at the RZPD Deutsches RessourcenZentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?clonID=DKFZp469A1622

Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

FEATURES

source

1. -739

/organism="Pongo pygmaeus"

/mol_type="mRNA"

/db_xref="txaxon:9606"

/clone="DKFZp469A1622"

/tissue_type="kidney"

/dev_stage="adult"

/lab_host="DNI0B"

/clone_lib="469 (synonym: pkid1)"

ORIGIN

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Best Local Similarity 98.8%; Pred. No. 4e-99; Mismatches 0; Indels 5; Gaps 0; Matches 397; Conservative 0; Insert Length: 529

QY 1 ATGCGCAATCCAAACATGCTGTTGACTCTATGATGCGCTTAACACTTCACAGATCCA 60

Db 327 ATGCGCAATCCAAACATGCTGTTGACTCTATGATGCGCTTAACACTTCACAGATCCA 386

QY 61 GCTTCGGAGAGAGAGACCTGTTGAGCAGGATGCTTGTGAAAGTTAAAGCT 120

Db 387 GCTTCGGAGAGAGACCTGTTGAGCAGGATGCTTGTGAAAGTTAAAGCT 446

QY 121 GTTGGTGACAAAGAGACCTATACATGAAAGGGTCTTTTATCCTGGCAGT 180

Db 447 GTTGGTGACAAAGAGACCTATACATGAAAGGGTCTTTTATCCTGGCAGT 506

QY 181 ATTAGACTAAACGATTATGATGAAACAAACATTTGTTATGTCATGAT 240

Db 507 ATTAGACTAAACGATTATGATGAAACAAACATTTGTTATGTCATGAT 566

QY 241 CTCTCTAGGAGATTGTTGGCGTGCACGGTCTCTGTGAAAGGACAGGAATAT 300

Db 567 CTCTCTAGGAGATTGTTGGCGTGCACGGTCTCTGTGAAAGGACAGGAATAT 625

QY 301 ACCATGATCTACAGGACTTGTAGTAGTCAATCGCAGGAATCATCGGACTCAGGTACA 360

Db 627 ACCATGATCTACAGAAGACTTGTAGTAGTCAATCGCAGGAATCATCGTACA 686

QY 361 TCTGTGAGTGTAGAACAGGTGTCACCTGAAAGGTGGAGCTAT 402

Db 687 TCTGTGAGTGTAGAACAGGTGTCACCTGAAAGGTGGAGCTAT 728

ORIGIN

Query Match 92.9%; Score 373.4; DB 7; Length 482;
Best Local Similarity 99.2%; Pred. No. 3e-93; Mismatches 0; Indels 2; Gaps 2; Matches 396; Conservative 0; Insert Length: 529

QY 6 CAATACCAACATGCTGTTACACTGTGATGCTGCTGTAACCACCTCACAGAT-CCAGT 63

Db 421 CAATACCAAAATGCTGCTGACTACTGTGATGCTGCTGTAACCACCTCACAGAT-CCAGT 362

QY 64 TCGGRACAAAGAGACCTGCTGTAGCACCAGGCTATGCTTGAAGTTATAAGTCTGTT 123

Db 361 TCGGRACAAAGAGACCCCTGGTAGACCACAGCATGCTTGAAGTTATAAGTCTGTT 302

QY 124 GGTGCAAAAGAGACCTATACATGAAAGAGGTTCTTTTATCCTGGCAGTATT 183

Db 301 GGTGCAAAAGAGACCTATACATGAAAGAGGTTCTTTTATCCTGGCAGTATT 242

QY 184 ATGACTAAACGATTATGATGAGAGCAACAAACATTTGTTATGTCATGCTT 243

Db 241 ATGACTAAACGATTATGATGAGAGCAACAAACATTTGTTATGTCATGCTT 182

QY 244 CTAGGAGATTGTTGGCTGCGTCCAGCTCTCTGTAAGAGACAGGAATATATAC 303

Db 181 CTAGGAGATTGTTGGCTGCGTCCAGCTCTCTGTAAGAGACAGGAATATATAC 122

QY 304 ATGATCTACAGGACTTGTAGTAGTCAATCGCAGGAATCATCGGACTCAGGTACTCT 363

Db 121 ATGATCTACAGGACTTGTAGTAGTCAATCGCAGGAATCATCGGACTCAGGTACTCT 62

QY 364 GTGAGTGTAGAACAGGTGTCACCTGAAAGGTGGAGTT 402

Db 61 GTGAGTGTAGAACAGGTGTCACCTGAAAGGTGGAGTT 23

RESULT 5

CO737650

LOCUS CO737650

DEFINITION S1H03c18d24f1 squirrel heart library 1 Spermophilus lateralis cDNA

ACCESSION CO737650

VERSION CO737650.1

KEYWORDS EST.

SOURCE

ORGANISM

KEYWORDS

EST.

REFERENCE

R80343.1 GI:856624

AUTHORS

1 (bases 1 to 482)

Hillier,L., Clark,N., Dubroque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucika,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohifing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and

Wilson,R.

The WashU-Merck EST Project

TITLE

UNpublished (1995)

COMMENT

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

TELE: 314 286 1800

FAX: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 529

High quality sequence stops: 371

Source: IMAGE Consortium, LBL

This clone is available royalty-free through LBL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Sq primer: M13R1
High quality sequence stop: 371.
FEATURES
Source

Location/Qualifiers

1..482

/note="Vector: psport1_Sfi; Site_1: SfiA; Site_2: SfiB"

ORIGIN

QY

/tissue_type="kidney"

/dev_stage="adult"

/lab_host="DNI0B"

/clone="469 (synonym: pkid1)"

/note="Vector: psport1_Sfi; Site_1: SfiA; Site_2: SfiB"

Sq primer: M13R1
High quality sequence stop: 371.
FEATURES
Source

Location/Qualifiers

1..482

/note="Organism: Homo sapiens"

/note="Sex: Female"

/note="Placenta obtained at birth (full term)"

/note="Lab host: Soares placenta Nb2HP"

/note="DB Xref: GDB:558688"

/note="DB Xref: taxon:9606"

/note="Note: "I-MAGE:147075"

/note="Organism: Homo sapiens"

/note="Polymerase: pt7r3d (Pharmacia) with a modified polylinker; Site 1: Not I - Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', AACTGGAAATTCGCGCCGGAGATTTTTTTTTTTTTTTT 3']"

/note="Double-stranded cDNA was ligated into Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pt7r3 vector. Library constructed by Bento Soares and M.Fatima Bonaldo. "

ORIGIN

Query Match 92.9%; Score 373.4; DB 7; Length 482;

Best Local Similarity 99.2%; Pred. No. 3e-93; Mismatches 0; Indels 2; Gaps 2; Matches 396; Conservative 0; Insert Length: 529

QY 6 CAATACCAACATGCTGTTACACTGTGATGCTGCTGTAACCACCTCACAGAT-CCAGT 63

Db 421 CAATACCAAAATGCTGCTGACTACTGTGATGCTGCTGTAACCACCTCACAGAT-CCAGT 362

QY 64 TCGGRACAAAGAGACCTGCTGTAGCACCAGGCTATGCTTGAAGTTATAAGTCTGTT 123

Db 361 TCGGRACAAAGAGACCCCTGGTAGACCACAGCTCTCTGTAAGGAGACAGGAATATAC 302

QY 124 GGTGCAAAAGAGACCTATACATGAAAGAGGTTCTTTTATCCTGGCAGTATT 183

Db 301 GGTGCAAAAGAGACCTATACATGAAAGAGGTTCTTTTATCCTGGCAGTATT 242

QY 184 ATGACTAAACGATTATGATGAGAGCAACAAACATTTGTTATGTCATGCTT 243

Db 241 ATGACTAAACGATTATGATGAGAGCAACAAACATTTGTTATGTCATGCTT 182

QY 244 CTAGGAGATTGTTGGCTGCGTCCAGCTCTCTGTAAGAGACAGGAATATAC 303

Db 181 CTAGGAGATTGTTGGCTGCGTCCAGCTCTCTGTAAGAGACAGGAATATAC 122

QY 304 ATGATCTACAGGACTTGTAGTAGTCAATCGCAGGAATCATCGGACTCAGGTACTCT 363

Db 121 ATGATCTACAGGACTTGTAGTAGTCAATCGCAGGAATCATCGGACTCAGGTACTCT 62

QY 364 GTGAGTGTAGAACAGGTGTCACCTGAAAGGTGGAGTT 402

Db 61 GTGAGTGTAGAACAGGTGTCACCTGAAAGGTGGAGTT 23

RESULT 5

CO737650

LOCUS CO737650

DEFINITION S1H03c18d24f1 squirrel heart library 1 Spermophilus lateralis cDNA

ACCESSION CO737650

VERSION CO737650.1

KEYWORDS EST.

SOURCE

ORGANISM

Spermophilus lateralis

Mammalia; Metacota; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;

Spermophilini.

1 (bases 1 to 779)

REFERENCE

Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W.,

Authors

Rogers,J. and Cossins,A.R.

TITLE	Microarray analysis of transcriptional changes during hibernation in the golden mantled ground squirrel, <i>Spermophilus lateralis</i>	ORGANISM	<i>Spermophilus lateralis</i>
JOURNAL	Unpublished (2004)	REFERENCE	Bukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae; <i>Spermophilus</i> ; 1 (bases 1 to 858)
COMMENT	Contact: Andrew R. Cossins Laboratory for Environmental Gene Regulation University of Liverpool School of Biological Sciences, The Biosciences Building, Crown Street, Liverpool, United Kingdom, L69 7ZB Tel: +44 (0)151-795-4510 Fax: +44 (0)151-795-4431 Email: cossins@liv.ac.uk Vector has been trimmed from this EST.	AUTHORS	Rogers, J. and Cossins, A.R. Microarray analysis of transcriptional changes during hibernation in the golden mantled ground squirrel, <i>Spermophilus lateralis</i>
FEATURES	Plate: 18 row: d column: 24 Seq primer: pfIC T7 (5'-ATACTGACTCACTATAGGG-3') High quality sequence stop: 779. Location/Qualifiers	JOURNAL	Unpublished (2004)
source	1. . . 779 /organism="Spermophilus lateralis" /mol_type="mRNA" /db_xref="taxon:76772" /clone="18d24" /sex="Male & female" /tissue_type="Heart" /dev_stages="Adult" /lab_host="E.coli Electromax DH10B" /clone_lib="Squirrel heart library 1" /note="Vector: pfIC; Site 1: Sall GTCGAG; Site 2: BamHI GCATCC; Normalized and subtracted cDNA library prepared from heart of hibernating and summer animals"	COMMENT	Contact: Andrew R. Cossins Laboratory for Environmental Gene Regulation University of Liverpool School of Biological Sciences, The Biosciences Building, Crown Street, Liverpool, United Kingdom, L69 7ZB Tel: +44 (0)151-795-4510 Fax: +44 (0)151-795-4431 Email: cossins@liv.ac.uk Vector has been trimmed from this EST.
ORIGIN	Query Match 91.2%; Score 366.8; DB 7; Length 779; Best Local Similarity 94.5%; Pred. No. 2.3e-91; Matches 380; Conservative 0; Mismatches 22; Indels 0; Gaps 0; QY 1 ATGTCGAATTCACAGATGCTGCTACTGATGCTGCTGAAAGCTCAACGATTCA 60 Db 125 ATGTCGAATTCACAGATGCTGCTACTGATGCTGCTGAAAGCTCAACGATTCA 184 QY 61 GCTTCGGAAACAGAGACCTCTGTTGAGCAACGCAATGCTGCTGAAAGCTCAACGATTCA 120 Db 185 GCTTCGGAAACAGAGACCTCTGTTGAGCAACGCAATGCTGCTGAAAGCTCAACGATTCA 244 QY 121 GCTTCGGAAACAGAGACCTCTGTTGAGCAACGCAATGCTGCTGAAAGCTCAACGATTCA 180 Db 245 GTTGGTGCAACAAAGACACTACATGAAAGAGGTATATTTTGTGCAAGT 304 QY 181 ATATGACTAAACGATTATGATGAGAACAAACATAATGATGATATGTCATAATGAT 240 Db 305 ATATGACTAAACGATTATGATGAGAACAAACATAATGATGATATGTCATAATGAT 364 QY 241 CTCTTAGGAGATTGTTGGGTGCAACGCTCTGTGAAAGAACAGAACAAATAT 300 Db 365 CTCTTAGGAGATTGTTGGGTGCAACGCTCTGTGAAAGAACAGAACAAATAT 424 QY 301 ACCATGATCTACAGAACTGCTGAGTAGTCATGAGCAGAACATCGGAGTCAGTCA 360 Db 425 ACAATGATCTACAAAAATTGTTGGGTGAACTACATGAGAACCACTCAGTCAGCACA 484 QY 361 TCTGTGAGTGAGAACAGGTGCACTTGAGGTTGGAGTGT 402 Db 485 TTAGTGAGTGAGAACAGGTGCACTTGAGGTTGGAGTGT 526 RESULT 6 Q7337954 Locus C0737954 Definition 858 bp mRNA linear EST 29-JUL-2004 Definition SLH03c19p19f1 squirrel heart library 1 <i>Spermophilus lateralis</i> cDNA Definition clone 19b19 5', mRNA sequence.	FEATURES	Plate: 19 row: b column: 19 Seq primer: pfIC T7 (5'-ATACTGACTCACTATAGGG-3') High quality sequence stop: 858. Location/Qualifiers
source	1. . . 858 /organism="Spermophilus lateralis" /mol_type="mRNA" /db_xref="taxon:76772" /clone="18p19" /sex="Male & female" /tissue_type="Heart" /dev_stages="Adult" /lab_host="E.coli Electromax DH10B" /clone_lib="Squirrel heart library 1" /note="Vector: pfIC; Site 1: Sall GTCGAG; Site 2: BamHI GCATCC; Normalized and subtracted cDNA library prepared from heart of hibernating and summer animals"	COMMENT	Contact: Andrew R. Cossins Laboratory for Environmental Gene Regulation University of Liverpool School of Biological Sciences, The Biosciences Building, Crown Street, Liverpool, United Kingdom, L69 7ZB Tel: +44 (0)151-795-4510 Fax: +44 (0)151-795-4431 Email: cossins@liv.ac.uk Vector has been trimmed from this EST.
ORIGIN	Query Match 91.2%; Score 366.8; DB 7; Length 858; Best Local Similarity 94.5%; Pred. No. 2.4e-91; Matches 380; Conservative 0; Mismatches 22; Indels 0; Gaps 0; QY 1 ATGTCGAATTCACAGATGCTGCTACTGATGCTGCTGAAAGCTCAACGATTCA 60 Db 160 ATGTCGAATTCACAGATGCTGCTACTGATGCTGCTGAAAGCTCAACGATTCA 219 QY 61 GCTTCGGAAACAGAGACCTCTGTTGAGCAACGCAATGCTGCTGAAAGCTCAACGATTCA 120 Db 220 GCTTCGGAAACAGAGACCTCTGTTGAGCAACGCAATGCTGCTGAAAGCTCAACGATTCA 279 QY 121 GCTTCGGAAACAGAGACCTCTGTTGAGCAACGCAATGCTGCTGAAAGCTCAACGATTCA 180 Db 280 GTTGGTGCAACAAAGACACTACATGAAAGAGGTCTTCTCTGGCCAGTAT 339 QY 181 ATATGACTAAACGATTATGATGAGAACAAACATAATGATGATATGTCATAATGAT 240 Db 340 ATATGACTAAACGATTATGATGAGAACAAACATAATGATGATATGTCATAATGAT 399 QY 241 CTCTTAGGAGATTGTTGGGTGCAACGCTCTGTGAAAGAACAGAACAAATAT 300 Db 400 CTCTTAGGAGATTGTTGGGTGCAACGCTCTGTGAAAGAACAGAACAAATAT 459 QY 301 ACCATGATCTACAGAACTGCTGAGTAGTCATGAGCAGAACATCGGAGTCAGTCA 360 Db 460 ACAATGATCTACAAAAATTGTTGGGTGAACTACATGAGAACCACTCAGTCAGCACA 519 RESULT 7 Q7337954 Locus C0737954 Definition 361 TCTGTGAGTGAGAACAGGTGCACTTGAGGTTGGAGTGT 402 Definition SLH03c19p19f1 squirrel heart library 1 <i>Spermophilus lateralis</i> cDNA Definition clone 19b19 5', mRNA sequence.	FEATURES	Plate: 19 row: b column: 19 Seq primer: pfIC T7 (5'-ATACTGACTCACTATAGGG-3') High quality sequence stop: 561. Location/Qualifiers
source	520 TTAGTGAGTGAGAACAGGTGCACTTGAGGTTGGAGTGT 561	COMMENT	Contact: Andrew R. Cossins Laboratory for Environmental Gene Regulation University of Liverpool School of Biological Sciences, The Biosciences Building, Crown Street, Liverpool, United Kingdom, L69 7ZB Tel: +44 (0)151-795-4510 Fax: +44 (0)151-795-4431 Email: cossins@liv.ac.uk Vector has been trimmed from this EST.
KEYWORDS	EST.	KEYWORDS	EST.
SOURCE	<i>Spermophilus lateralis</i> (golden-mantled ground squirrel)	SOURCE	BB900427

ORIGIN

Query Match 80.7%; Score 324.4; DB 2; Length 345; Best Local Similarity 98.2%; Pred. No. 1.4e-79; Matches 328; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGGCAATACCAACATGCTGTTACTGATGCTGCTGAAACCTCCACAGATCCA 60

Db 12 AGGGCAATACCAACATGCTGTTACTGATGCTGCTGAAACCTCCACAGATCCA 71

QY 61 GCTTCGAAACAGAGACCTGGTTAGACCAAGCCATTGCTTGAAGTTAAAGCT 120

Db 703 TTAGTGAGTGAACAGGTTGCCACCT 728

RESULT 9

BE765314 Locus BR765314 345 bp mRNA linear EST 19-SBP-2000 Definition NT0102-280700-115-H11 NT0102 Homo sapiens cDNA, mRNA sequence. Accession BR765314.1 Version EST. Keywords SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bivalvia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1. (bases 1 to 345)

AUTHORS Nádas Neto,E., Garcia Correa,R., Veriowski-Almeida,S., Briones,M.R., Nágai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Mattsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed Sequence tag

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10731800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antônio Prudente 109, 4 andar, 01509-010, São Paulo-SP, Brazil

Tel: +55-11-2707001

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL: <http://www.ludwig.org.br/scripts/gethtml2.pl?tl=at2=IL2-NT0102-280700-15-H11&t3=2000-07-28&t4=1>

Seq primer: puc 18 forward

High quality sequence start: 14

High quality sequence stop: 344.

Location/Qualifiers

1. -345

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="txon:9606"

/dev_stage="Adult"

/clone.Lib="NT0102"

/note="Organ: nervous tumor; Vector: puc18; Site_1: SfIa; Site_2: SmaI; A mini-library was made by cloning products derived from ORISTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES source

ORIGIN

Query Match 80.6%; Score 324; DB 1; Length 393; Best Local Similarity 99.4%; Pred. No. 1.8e-79; Matches 324; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCAATACCAACATGCTGTTACTGATGCTGCTGAAACCTCCACAGATCCA 60

Db 68 ATGGCAATACCAACATGCTGTTACTGATGCTGCTGAAACCTCCACAGATCCA 127

QY 61 GCTTCGAAACAGAGACCTGGTTAGACCAAGCCATTGCTTGAAGTTAAAGCT 120

Db 72 GCTTCGAAACAGAGACCTGGTTAGACCAAGCCATTGCTTGAAGTTAAAGCT 131

QY 121 GTCGGTGCACAAAGACCTTATACTATGAANGAGGTTCTTCTTGCACGAT 180

Db 132 GCTGATGCACAAAGACCTTATACTATGAAGGAGCTTCTTCTTGCACGAT 191

QY 181 ATTATGACTAACGATTATATGAGAGAACATATGATATGTCGAATGAT 240

Db 192 ATTATGACTAACGATTATATGATGAGAACACATATGTCGAATGTCGAATGAT 251

QY 241 CTTCAGGAGATTGTTGGCGGCCAGCTTCTGGAAGAGCAGGAATAT 300

Db 252 CTCTAGGAGATTGTTGGCGGCCAGCTTCTGGAAGAGCAGGAATAT 311

QY 301 ACCATGATCTACGAGACTGTGGTTAGACCAAGCCATTGCTTGAAGTTAAAGCT 334

Db 312 ACCATGATCTACGAGACTGTGGTTAGACCAAGCCATTGCTTGAAGTTAAAGCT 345

RESULT 10

AI704062 Locus AL704062-1428 r1 393 bp mRNA linear EST 04-SBP-2003 Definition DKFZp686N1428 5', mRNA sequence. Accession AL704062.1 Version GR:19684717

KEYWORDS EST.

ORGANISM Homo sapiens (human)

Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bivalvia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1. (bases 1 to 393)

AUTHORS Ottenwaelder,B., Obermaier,B., Meves,W., Meves,H.W., Weil,B. and Wiemann,S.

TITLE EST (Ottenwaelder,B., Obermaier,B., Meves,W., Meves,H.W., Weil,B. and Wiemann,S.) Unpublished (2001)

COMMENT Contact: MIPS

FEATURES source

ORIGIN

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert.

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Mannheim) (Germany) within the cDNA sequencing consortium of the German Genome Project. No 81 sequence available. This clone (DKFZp686N1428) is available at the RZPD in Berlin. Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers

1. -393

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9605"

/clone.Lib="NT0102"

/note="Vector: priblplex2; site_1: SfIa; site_2: SfIb; cDNA-collection"

FEATURES source

ORIGIN

Query Match 80.6%; Score 324; DB 1; Length 393; Best Local Similarity 99.4%; Pred. No. 1.8e-79; Matches 324; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCAATACCAACATGCTGTTACTGATGCTGCTGAAACCTCCACAGATCCA 60

Db 68 ATGGCAATACCAACATGCTGTTACTGATGCTGCTGAAACCTCCACAGATCCA 127

QY 61 GCTTCGAAACAGAGACCTGGTTAGACCAAGCCATTGCTTGAAGTTAAAGCT 120

Best Local Similarity 89.9%; Pred. No. 9e-78; Score 318; DB 1; Length 518; Query Match

RESULT 11

Db 128 GCTTCGGAAAGAGAGACCTGTTGAGCCAAAGCCATTGCTTGAAGTTAAAGCT 187
 Qy 121 GTTGTGCAACAAAGAGACCTATCTATGAAAGAGGTCTTATCTGGCAGT 180
 Db 188 GNNGTGCAACAAAGAGACCTATCTATGAAAGAGGTCTTATCTGGCAGT 247
 Qy 181 ATTAGCTAAACGATTATGTAGAGACACATATGTTCAATGAT 240
 Db 248 ATTAGCTAAACGATTATGTAGAGACACATATGTTCAATGAT 307
 Qy 241 CTCCTAGGAGATTGTCGGTGCAGGTCTGTGAAAGAGCACAGGAATAT 300
 Db 308 CTCCTAGGAGATTGTCGGTGCAGGTCTGTGAAAGAGCACAGGAATAT 367
 Qy 301 ACCATGATCTACAGAACTTGTGACT 366
 Db 368 ACCATGATCTACAGAACTTGTGACT 393

REFERENCE

Db 1902188/C

LOCUS

DEFINITION

VERSION

KEYWORDS

ORGANISM

SOURCE

REMARKS

Db 1902188

518 bp mRNA linear EST 30-MAR-2000

III-BT002-221198-015 BT002 Homo sapiens cDNA, mRNA sequence.

AI902188.1 GI:6492666

EST.

Homo sapiens (human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. (bases 1 to 518)

Authors

Das Neto, E., Garcia Correa, R., Veriovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baita, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Simpson, A.J., Sores, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Hare, M.J.

Title

Journal

Medline

Pubmed

Comment

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2707922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/seq/gethtml.p?l1=IL&t2=11-BT002-015.html&t3=221198t4=1>)

Seq primer: puc 18 forward.
 Location/Qualifiers

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 /sex="female"
 /dev_stage="adult"
 /clone_lib="BT002"
 /incub="Organ: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

RESULT 12

Db 3409877

LOCUS

DEFINITION

VERSION

KEYWORDS

ORGANISM

REFERENCE

Authors

Title

Journal

Comment

Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 400 Std Error: 0.00.

FEATURES

source

1. -400
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells"
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ORIGIN

Query Match

79.1%; Score 318; DB 1; Length 518;

/lab_host="DHL0B"
 /clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"

/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro.

Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 333208-325895 Soares Nb2HP pool 1: 145032-147335, 14770-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HP-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322223, 326280-32663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 73.3%; Score 294.6; DB 2; Length 507;
 Best Local Similarity 95.6%; Pred. No. 3.1e-71; Matches 303; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGTCGAATCCACATGCTGACTACTGATGGTCGCTAACACCTCACAGTTCA 60
 Db 185 ATGTCGAATCCACATGCTGACTACTGATGGTCGCTAACACCTCACAGTTCA 244
 Qy 61 GCTTGGAAAGAGAACCTGGTAGACCAAGACGATGTTGAGTTAAGTCT 120
 Db 245 GCTTGGAAAGAGAACCTGGTAGACCAAGACGATGTTGAGTTAAGTCT 304
 Qy 121 GTTGGTGCACAAAGAACACTTATCTATGAGGTTCTTTTATCTGSCAGAT 180
 Db 305 GTTGGTGCACAAAGAACACTTATCTATGAGGTTCTTTTATCTGSCAGAT 364
 Qy 181 ATTAGACTAACGTTATGATGAGAACAGAACATTTGATATTTCAATGAT 240
 Db 365 ATTATGACTAACGTTATGATGAGAACAGAACATTTGATATTTCAATGAT 424
 Qy 241 CTCTAGGAGATTGTTGGGTGCGCAAGCTCTGTGAGAGCACGGAAATAT 300
 Db 425 CTCTAGGAGATTGTTGGGTGCGCAAGCTCTGTGAGAGCACGGAAATAT 484
 Qy 301 ACCATGATCTACAGGA 317
 Db 485 AGTTAGTCATGTAA 501

ORIGIN

Query Match 73.3%; Score 294.6; DB 2; Length 512;
 Best Local Similarity 95.6%; Pred. No. 3.1e-71; Matches 303; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGTCGAATCCACATGCTGACTACTGATGGTCGCTAACACCTCACAGTTCA 60
 Db 186 ATGTCGAATCCACATGCTGACTACTGATGGTCGCTAACACCTCACAGTTCA 245
 Qy 61 GCTTGGAAAGAGAACCTGGTAGACCAAGACGATGTTGAGTTAAGTCT 120
 Db 246 GCTTGGAAAGAGAACCTGGTAGACCAAGACGATGTTGAGTTAAGTCT 305
 Qy 121 GTTGGTGCACAAAGAACACTTATCTATGAGGTTCTTTTATCTGSCAGAT 180
 Db 306 GTTGGTGCACAAAGAACACTTATCTATGAGGTTCTTTTATCTGSCAGAT 365
 Qy 181 ATTAGACTAACGTTATGATGAGAACAGAACATTTGATATTTCAATGAT 240
 Db 366 ATTATGACTAACGTTATGATGAGAACAGAACATTTGATATTTCAATGAT 425
 Qy 241 CTCTAGGAGATTGTTGGGTGCGCAAGCTCTGTGAGAGCACGGAAATAT 300
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FEATURES

Location/Qualifiers
 1. .512

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 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI;

/mol_type="mRNA" /db_xref="IMGR:368555" .

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/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro.

Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 333208-325895 Soares Nb2HP pool 1: 145032-147335, 14770-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HP-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 304776-306311, 320136-322223, 326280-32663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 73.3%; Score 294.6; DB 2; Length 507;
 Best Local Similarity 95.6%; Pred. No. 3.1e-71; Matches 303; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGTCGAATCCACATGCTGACTACTGATGGTCGCTAACACCTCACAGTTCA 60
 Db 185 ATGTCGAATCCACATGCTGACTACTGATGGTCGCTAACACCTCACAGTTCA 244
 Qy 61 GCTTGGAAAGAGAACCTGGTAGACCAAGACGATGTTGAGTTAAGTCT 120
 Db 245 GCTTGGAAAGAGAACCTGGTAGACCAAGACGATGTTGAGTTAAGTCT 304
 Qy 121 GTTGGTGCACAAAGAACACTTATCTATGAGGTTCTTTTATCTGSCAGAT 180
 Db 305 GTTGGTGCACAAAGAACACTTATCTATGAGGTTCTTTTATCTGSCAGAT 364
 Qy 181 ATTAGACTAACGTTATGATGAGAACAGAACATTTGATATTTCAATGAT 240
 Db 365 ATTATGACTAACGTTATGATGAGAACAGAACATTTGATATTTCAATGAT 424
 Qy 241 CTCTAGGAGATTGTTGGGTGCGCAAGCTCTGTGAGAGCACGGAAATAT 300
 Db 425 CTCTAGGAGATTGTTGGGTGCGCAAGCTCTGTGAGAGCACGGAAATAT 484
 Qy 301 ACCATGATCTACAGGA 317
 Db 485 AGTTAGTCATGTAA 501

ORIGIN

Query Match 73.3%; Score 294.6; DB 2; Length 512;
 Best Local Similarity 95.6%; Pred. No. 3.1e-71; Matches 303; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGTCGAATCCACATGCTGACTACTGATGGTCGCTAACACCTCACAGTTCA 60
 Db 186 ATGTCGAATCCACATGCTGACTACTGATGGTCGCTAACACCTCACAGTTCA 245
 Qy 61 GCTTGGAAAGAGAACCTGGTAGACCAAGACGATGTTGAGTTAAGTCT 120
 Db 246 GCTTGGAAAGAGAACCTGGTAGACCAAGACGATGTTGAGTTAAGTCT 305
 Qy 121 GTTGGTGCACAAAGAACACTTATCTATGAGGTTCTTTTATCTGSCAGAT 180
 Db 306 GTTGGTGCACAAAGAACACTTATCTATGAGGTTCTTTTATCTGSCAGAT 365
 Qy 181 ATTAGACTAACGTTATGATGAGAACAGAACATTTGATATTTCAATGAT 240
 Db 366 ATTATGACTAACGTTATGATGAGAACAGAACATTTGATATTTCAATGAT 425
 Qy 241 CTCTAGGAGATTGTTGGGTGCGCAAGCTCTGTGAGAGCACGGAAATAT 300
 Db 426 CTCTAGGAGATTGTTGGGTGCGCAAGCTCTGTGAGAGCACGGAAATAT 485

Search completed: October 18, 2004, 14:51:57

Job time : 7339 secs

RESULT 15
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 DEFINITION nab4310.1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
 IMAGE 3268955 3, similar to SW_MDM2_HUMAN Q00987 MDM2 PROTEIN ;,
 ACCESSION BF435134.1 GI:11447422
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 MmRNA sequence.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 512)
 AUTHORS NCI-NCAP http://www.ncbi.nlm.nih.gov/nci-cgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapb@mail.nih.gov
 This clone is available royalty-free through LInL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: -40UP from Gibco
 High quality sequence stop: 452..

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